

Insect survey 2020, basic analysis

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To-do * Remove extra lysation samples!!! Some samples got two runs, with two lysate runs	
• These species are not matched to the gyldig names in artsdatabasen yet.	
• Should store dates and times separately as well in logger_data table. Easier to subset later.	

- Notera i rapport hur många treffer som er misstenkte.
- Make plots of phenology
 - No. species over the season for each location. Split into separate figs for the two habitats?
 - Relate this to local temperature, temperature sums?
- Plots of number of samples over time
- Check differences btw 2 week and 4 week sampling
 - Compare first and second of the 2 weeks, see if any of the have more overlap with 4 week. If 4 week becomes full, the first 2 week period should overlap more.
 - Do this for window traps as well.
- Within habitat, check relationship btw species richness and a few variables
 - Forest age
 - Diversity of fauna
 - Temperature
 - Altitude

Data import and cleaning

At this point I get the raw data from Marie, which requires some cleaning. In the future, we'll put this all in a database, and separate out the cleaning and database import in a separate script.

```
#dat <- read_delim("../Data/Genetikkdata/long_format_data_GCF-2020-735_736_19102020.txt",
#  as.tibble()

#dat <- read_delim("../Data/Genetikkdata/long_format_data_GCF-2020-735_736_19102020.txt")

dat <- read_delim("../Data/Genetikkdata/long_format_data_GCF-2020-735_736_744_26102020.txt",
  delim = ";",
  col_types = cols(
    kingdom = col_character(),
    phylum = col_character(),
    class = col_character(),
    order = col_character(),
    family = col_character(),
    genus = col_character(),
    species = col_character(),
    sample = col_character(),
    value = col_double(),
    GenlabID = col_character(),
```

```

GUID = col_character(),
Tilsatt_antall_C.analis_SI_USA_08.06.20 = col_double(),
Tilsatt_antall_C.chinensis_08.06.20 = col_double(),
Tilsatt_antall_Sirisser = col_double(),
Tilsatt_antall_Melormer = col_double(),
Tilsatt_antall_C.maculatus = col_double(),
Vekt_tom_flaske_.g. = col_double(),
Vekt_flaske_med_EtOH_og_insekter_.g. = col_double(),
Vekt_flaske_._insekter_vaat_.g. = col_double(),
Vekt_flaske_._insekter_toerr_.g. = col_double(),
Totalvolum_.mengde_ATL_._prot.K_mL. = col_character(),
Vaatvekt_.g. = col_double(),
Toerrvekt_.g. = col_double(),
Kommentar_proeve = col_character(),
Ekstraksjonsdato = col_date(format = "%d.%m.%Y"),
Ekstraksjonskit = col_character(),
Subsamplet_volum_.ul. = col_double(),
Elueringsvolum = col_double(),
OD = col_double(),
X260_280 = col_double(),
X260_230 = col_double(),
Labperson = col_character(),
Ekstraksjonskommentar = col_character(),
locality = col_character(),
trap = col_character(),
date_placed = col_date(format = "%d.%m.%Y"),
time_placed = col_time(format = ""),
empty_week = col_double(),
dateemptied = col_date(format = "%d.%m.%Y"),
timeemptied = col_time(format = ""),
liquid = col_character(),
personemptied = col_character(),
sample_id = col_character(),
mottat_lab = col_character(),
comment = col_character()
),
na = c("NA",
      "N/A",
      "Maa veies"
)
)
)

```

Fix some coding errors.

```

# dat %>%
#   select(genus, species, new_species) %>%

```

```

# slice(297, 1902)
#
#
# dat %>%
#   select(genus, species, new_species) %>%
# slice(3219, 3585, 4017, 11424, 13275, 15465, 21056, 24168, 25077, 31567, 32805, 48502, 49
#
#Ekstraksjonskommentar = gsub(pattern = "[\\\"]", "", Ekstraksjonskommentar),
dat <- dat %>%
  mutate(species_latin = species)

dat <- dat %>%
  mutate(species = gsub(" sp", "_sp", species))

dat <- dat %>%
  mutate(species = gsub("[0-9](_)(sp)", "\\\\[1]\\3", species))

dat <- dat %>%
  mutate(species = gsub("(.*)(_)(.*)", "\\3", species))

dat <- dat %>%
  mutate(locality = str_to_sentence(locality))

```

Set factor levels

```

dat <- dat %>%
  mutate(locality = factor(locality, levels = c(paste0("Semi-nat_", 1:10), paste0("Skog_", 1
trap_type = ifelse(grepl("MF", trap), "Malaise", "Vindu"),
habitat_type = ifelse(grepl("Skog", locality), "Skog", "SN_Gressmark"),
liquid = ifelse(grepl("etoh85", liquid), "Ethanol", "PropGl_Ethanol"),
weeks_sampled = ifelse(grepl("1", trap) | grepl("3", trap), 2, 4)
)
```

Write a species list for the entomologists

```

dat %>%
  select(kingdom,
phylum,
class,
order,
family,
genus,
species) %>%

```

```

distinct() %>%
arrange(kingdom,
        phylum,
        class,
        order,
        family,
        genus,
        species) %>%
write_excel_csv(path = "out/species_list_2020-11-02.csv")

## Warning: The `path` argument of `write_excel_csv()` is deprecated as of readr 1.4.0.
## Please use the `file` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was generated.

```

Filter out the Nerlandsøya samples

```

dat <- dat %>%
  filter(locality != "Nerlandsoeya") %>%
  droplevels()

```

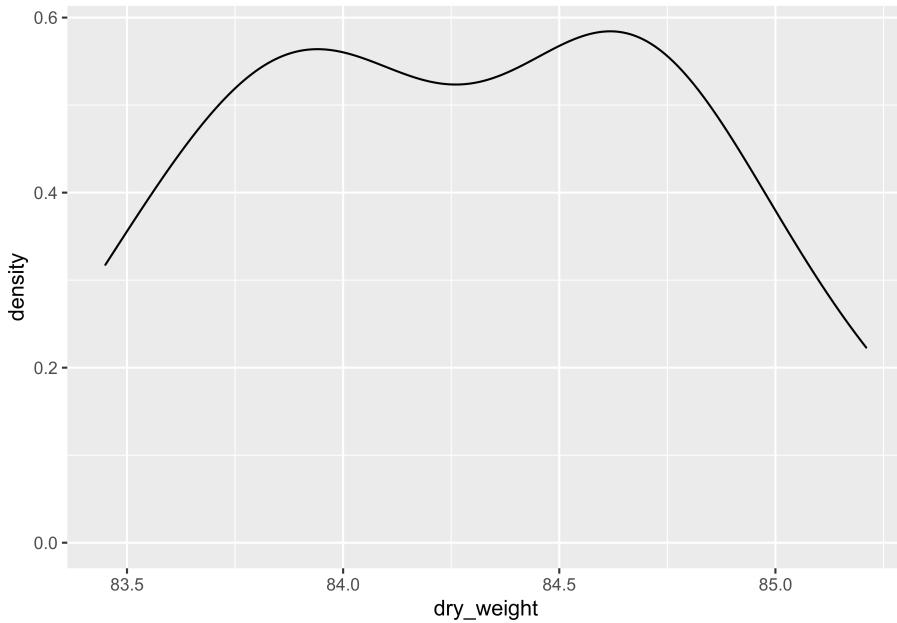
Add missing bottle weights. This is based on a sample of bottle dry weight measurements made after the regular weighings.

```

bottle_weights <- tbl(con,
                      in_schema("catch_data", "bottle_weights")) %>%
  select(-id)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)
bottle_weights %>%
  filter(bottle_type == "MF" & year == 2000) %>%
  select(dry_weight) %>%
  ggplot(.) +
  geom_density(aes(x = dry_weight))

```



```

bottle_weights_MF <- bottle_weights %>%
  filter(bottle_type == "MF" & year == 2000) %>%
  select(dry_weight) %>%
  summarize(mean_weight = mean(dry_weight)) %>%
  collect()

## Warning: Missing values are always removed in SQL.
## Use `mean(x, na.rm = TRUE)` to silence this warning
## This warning is displayed only once per session.

sum(is.na(dat$Vekt_tom_flaske_.g.))

## [1] 6572

dat <- dat %>%
  mutate(Vekt_tom_flaske_.g. = ifelse(trap_type == "Malaise" & is.na(Vekt_tom_flaske_.g.), NA, Vekt_tom_flaske_.g.))

sum(is.na(dat$Vekt_tom_flaske_.g.))

## [1] 1368

dat <- dat %>%
  mutate(Vaatvekt_.g. = Vekt_flaske_..insekter_vaat_.g. - Vekt_tom_flaske_.g.,
         Toerrvekt_.g. = Vekt_flaske_..insekter_toerr_.g. - Vekt_tom_flaske_.g.)

```

Check the emptying dates.

The dates seems to be OK this time. Should do a proper check on the endpoints though.

```
dat <- dat %>%
  mutate(days_collected = as.numeric(dat$date_emptied - dat$date_placed))

# dat %>%
#   filter(days_collected == 0) %>%
#   select(sample_id,
#         GUID,
#         date_placed,
#         date_emptied) %>%
#   distinct() %>%
#   print(n = Inf)
#
# hist(as.numeric(dat$date_emptied - dat$date_placed))

dat %>%
  group_by(days_collected) %>%
  summarise(n())

## `summarise()` ungrouping output (override with `.`groups` argument)

## # A tibble: 16 x 2
##   days_collected `n()`
##   <dbl> <int>
## 1 10     368
## 2 11    1084
## 3 12    5654
## 4 13    6223
## 5 14   10831
## 6 15    8053
## 7 16   11159
## 8 17    1422
## 9 25    561
## 10 26   1101
## 11 27   3016
## 12 28   9687
## 13 29   1132
## 14 30    450
## 15 31   1175
## 16 32    734

# dat %>%
#   filter(days_collected == 8) %>%
```

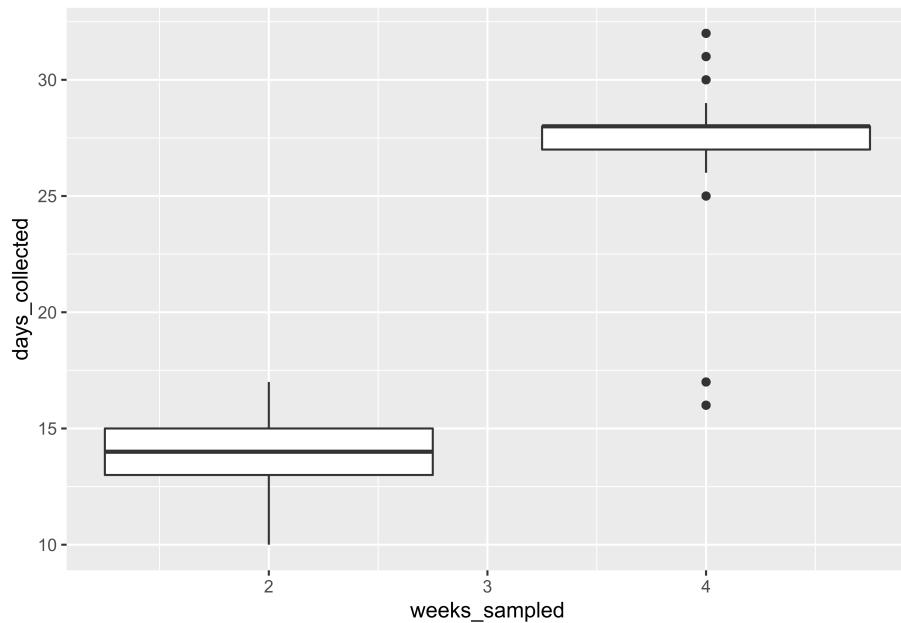
```

#   select(sample_id,
#          GUID,
#          date_placed,
#          date_emptied) %>%
#  distinct() %>%
#  print(n = Inf)

```

Set weeks sampled manually for the few locations in Oslo that got an extra short sampling in the beginning.

```
ggplot(dat, aes(x = weeks_sampled, y = days_collected, group = weeks_sampled)) +
  geom_boxplot()
```



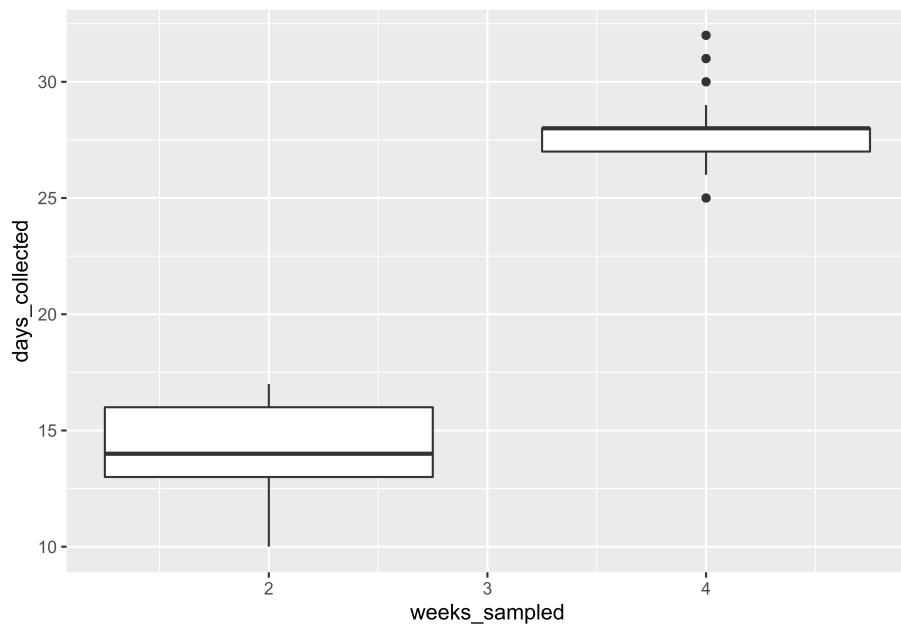
```

twoWeeks <- dat %>%
  filter(weeks_sampled == 4 &
         days_collected < 20) %>%
  select(sample_id) %>%
  distinct() %>%
  as.vector()

dat <- dat %>%
  mutate(weeks_sampled = ifelse(sample_id %in% twoWeeks[[1]], 2, weeks_sampled))

ggplot(dat, aes(x = weeks_sampled, y = days_collected, group = weeks_sampled)) +
  geom_boxplot()

```



Check missing weight data

```

dat %>%
  group_by(empty_week) %>%
  select(Vekt_tom_flaske_.g.,
         Vekt_flaske_med_EtOH_og_insekter_.g.,
         Vekt_flaske_.insekter_vaat_.g.,
         Vekt_flaske_.insekter_toerr_.g.,
         Vaatvekt_.g.,
         Toerrvekt_.g.)
  ) %>%
  distinct() %>%
  summarise_all(~sum(is.na(.)))

```

Adding missing grouping variables: `empty_week`

	empty_week	Vekt_tom_flaske~	Vekt_flaske_med~	Vekt_flaske_.i~	Vekt_flaske_.i~
	<dbl>	<int>	<int>	<int>	<int>
## 1	22	6	0	0	0
## 2	24	20	0	0	0
## 3	26	10	3	0	2

```

## 4      28      4      9      0      0
## 5      30      2      2      0      2
## 6      32      0      0      0      0
## # ... with 2 more variables: Vaatvekt_.g. <int>, Toerrvekt_.g. <int>

```

Summaries of samples

Total weight of insect catches.

```

dat %>%
  group_by(sample_id) %>%
  summarise(dry_weight = mean(Toerrvekt_.g., na.rm = T),
             wet_weight = mean(Vaatvekt_.g., na.rm = T)) %>%
  summarise(tot_dry_weight = sum(dry_weight, na.rm = T),
             tot_wet_weight = sum(wet_weight, na.rm = T))

## `summarise()` ungrouping output (override with `.`groups` argument)

## # A tibble: 1 x 2
##   tot_dry_weight tot_wet_weight
##       <dbl>          <dbl>
## 1     1460.        6249.

```

Total number of taxa

```

dat %>%
  summarise(no_taksa = n_distinct(order, family, genus, species))

## # A tibble: 1 x 1
##   no_taksa
##       <int>
## 1     10092

```

Basic species richness graphs

Quick look at diversity at the different sites.

```

total_no_taxa <- dat %>% select(order, family, genus, species) %>%
  distinct() %>%
  count()

dat %>%
  filter(grepl("MF", trap)) %>%
  group_by(locality, habitat_type) %>%
  select(genus, species, habitat_type) %>%
  distinct() %>%

```

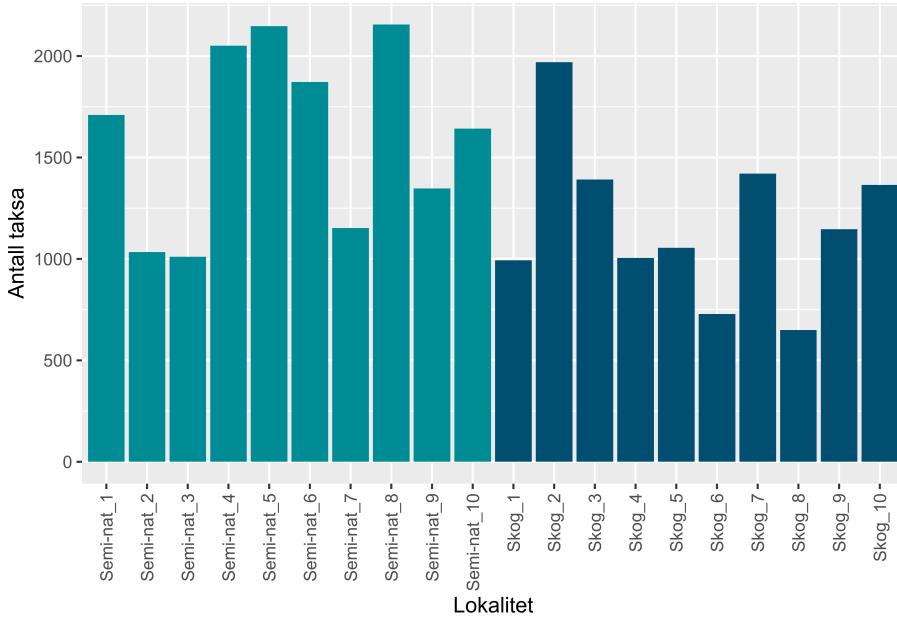


Figure 1: Cumulative number of taxa found in malaise traps.

```

count() %>%
ungroup() %>%
ggplot(.) +
  geom_bar(aes(y = n, x = locality, fill = habitat_type),
           stat = "identity") +
# ggtitle(paste0("Kumulativ artsrikedom i\nalle malaisefeller per ", max(dat$dateemptied)),
#         theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1),
#               legend.position = "none") +
#         scale_fill_nina() +
#         ylab("Antall taksa") +
#         xlab("Lokalitet"))

## Adding missing grouping variables: `locality`
dat %>%
  filter(grepl("VF", trap)) %>%
  group_by(locality, habitat_type) %>%
  select(genus, species) %>%
  distinct() %>%
  count() %>%
  ungroup() %>%
  ggplot(.) +

```

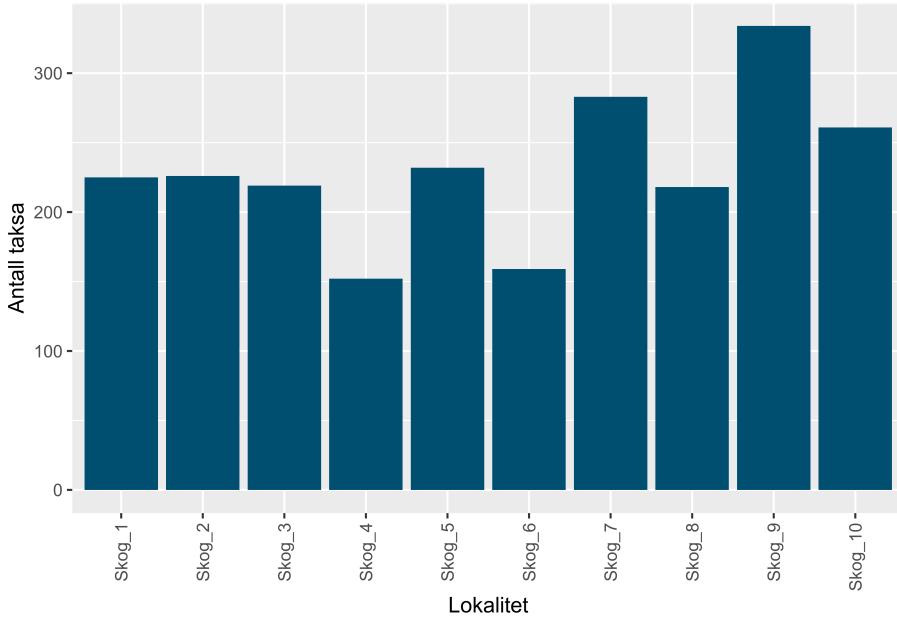


Figure 2: Cumulative number of taxa found in window traps.

```

geom_bar(aes(y = n, x = locality, fill = habitat_type),
         stat = "identity") +
# ggttitle(paste0("Kumulativ artsrikedom i\nalle vindusfeller per ", max(dat$dateemptied),
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1),
        legend.position = "none") +
  scale_fill_nina() +
  ylab("Antall taksa") +
  xlab("Lokalitet")

## Adding missing grouping variables: `locality`, `habitat_type`
```

Basic biomass graphs

NB, we still have some missing data on the weight of the bottles.

Quick quality check of the spread of the bottle weights. Could we impute the missing values?

```

dat %>%
  select(Vekt_tom_flaske_.g.,
         Vekt_flaske_med_EtOH_og_insekter_.g.,
```

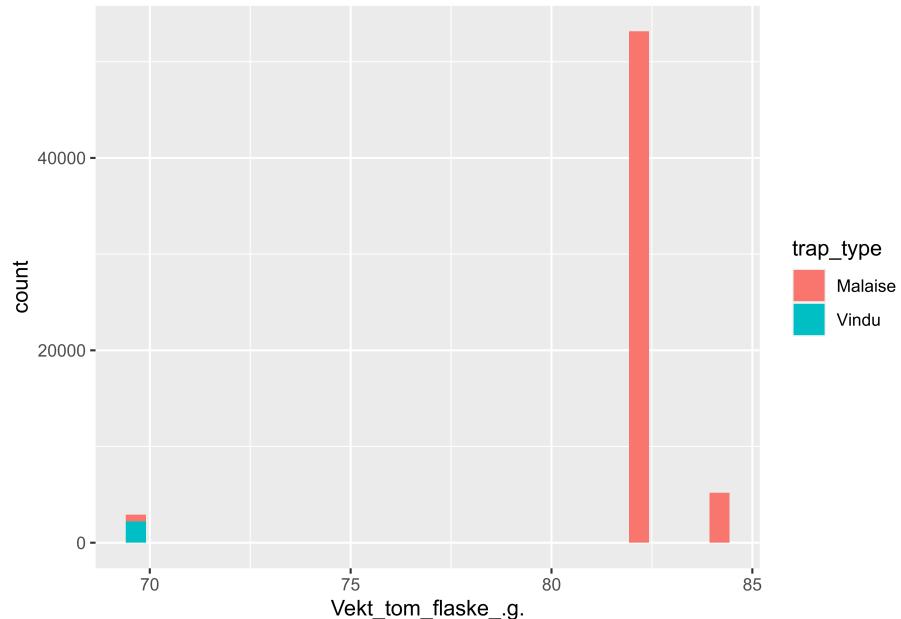
```

Vekt_flaske_._insekter_vaat_.g.,
Vekt_flaske_._insekter_toerr_.g.,
Vaatvekt_.g.,
Toerrvekt_.g.)

## # A tibble: 62,650 x 6
##   Vekt_tom_flaske~ Vekt_flaske_med~ Vekt_flaske_._i~ Vekt_flaske_._i~
##   <dbl>           <dbl>           <dbl>           <dbl>
## 1 82.2            728             118.            89.0
## 2 82.2            728             118.            89.0
## 3 82.2            728             118.            89.0
## 4 82.2            728             118.            89.0
## 5 82.2            728             118.            89.0
## 6 82.2            728             118.            89.0
## 7 82.2            728             118.            89.0
## 8 82.2            728             118.            89.0
## 9 82.2            728             118.            89.0
## 10 82.2           728             118.            89.0
## # ... with 62,640 more rows, and 2 more variables: Vaatvekt_.g. <dbl>,
## #   Toerrvekt_.g. <dbl>
ggplot(dat) +
  geom_histogram(aes(Vekt_tom_flaske_.g., fill = trap_type))

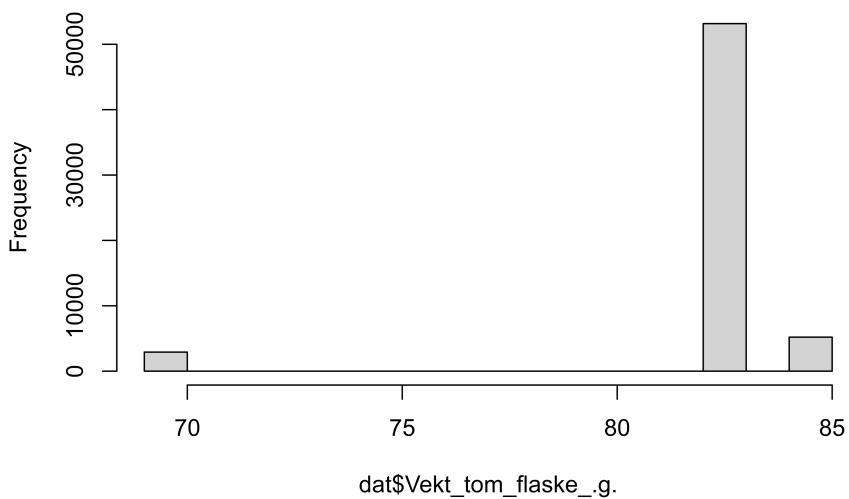
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## Warning: Removed 1368 rows containing non-finite values (stat_bin).

```



```
hist(dat$Vekt_tom_flaske_.g.)
```

Histogram of dat\$Vekt_tom_flaske_.g.



```
table(dat$Vekt_tom_flaske_.g.)
```

```
##
```

```

##          69.75      82.21      82.2103 84.2816666666667
##          2915      40333     12830      5204

```

These bottle weights are weirdly consistent. Did they really weigh all bottles?
UPDATE WITH NEW BOTTLE WEIGHTS. !!DONE!!

```
summary(dat$Toerrvekt_.g.)
```

```

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
## -0.57    4.84   8.33  13.61  16.17  80.35  4207

```

Quick look at the biomass at the different sites.

```

dat %>%
  filter(grepl("MF", trap)) %>%
  group_by(locality, habitat_type) %>%
  ggplot(.) +
  geom_boxplot(aes(y = Toerrvekt_.g., x = locality, fill = habitat_type)) +
  # ggtitle(paste0("Middels avrunnen vekt (pluss flaske)\nav insekter i malaisefeller per ",
  # theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1),
  #       legend.position = "none") +
  #       scale_fill_nina() +
  ylab("Vekt (g.)") +
  xlab("Lokalitet")

```

```
## Warning: Removed 2839 rows containing non-finite values (stat_boxplot).
```

```

dat %>%
  filter(grepl("VF", trap)) %>%
  group_by(locality, habitat_type) %>%
  ggplot(.) +
  geom_boxplot(aes(y = Toerrvekt_.g., x = locality, fill = habitat_type)) +
  #ggtitle(paste0("Middels avrunnen vekt (pluss flaske) av insekter i\nvindusfeller per ", r
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1),
        legend.position = "none") +
        scale_fill_nina() +
        ylab("Vekt (g.)") +
        xlab("Lokalitet")

```

```
## Warning: Removed 1368 rows containing non-finite values (stat_boxplot).
```

Check overlap between malaise and window traps

Simple: total spec richn for all traps and times per location, plus the same for just malaise and window traps. group in figure by location

complex: tally how many spec is found in only one trap type. No unnecessary

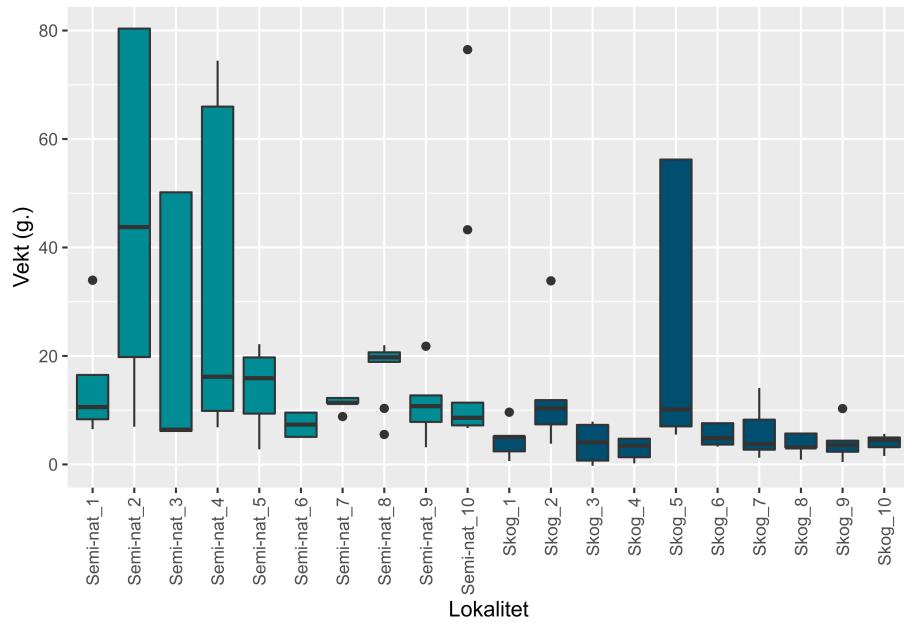


Figure 3: Average biomass (dry weight) in malaiase traps.

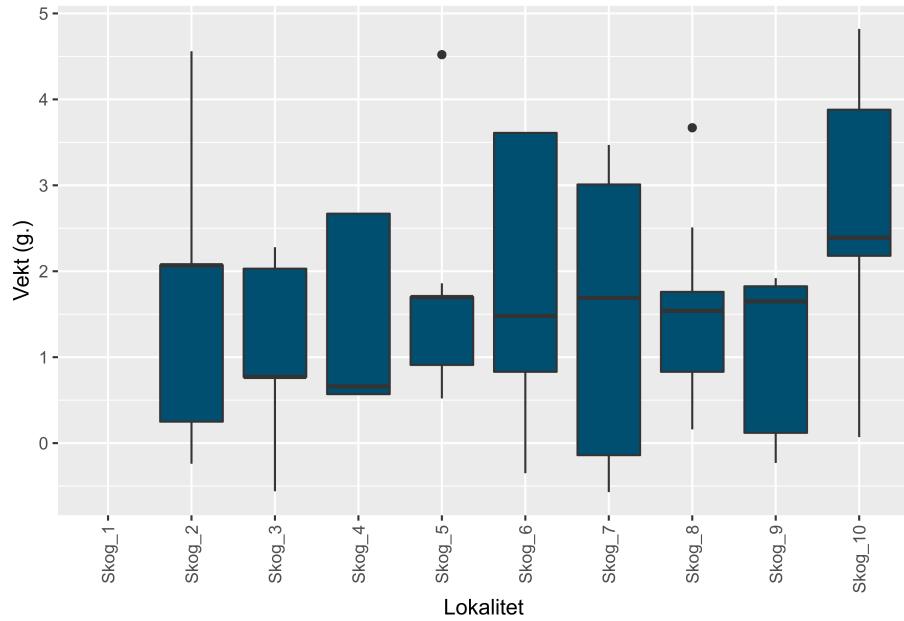


Figure 4: Average biomass (dry weight) in window traps.

per species: which sp is only found in one trap type. or per species, % of findings in each trap type

Total number of coleoptera species per trap type

```
col_spec_richn_tot <- dat %>%
  filter(order == "Coleoptera",
         habitat_type == "Skog") %>%
  group_by(locality) %>%
  summarise(col_spec_richn = n_distinct(genus, species)) %>%
  mutate(trap_type = "Alle")

## `summarise()` ungrouping output (override with `.`groups` argument)
col_spec_richn_trap <- dat %>%
  filter(order == "Coleoptera",
         habitat_type == "Skog") %>%
  group_by(locality,
           trap_type) %>%
  summarise(col_spec_richn = n_distinct(genus, species))

## `summarise()` regrouping output by 'locality' (override with `.`groups` argument)
col_spec_richn <- col_spec_richn_tot %>%
  union_all(col_spec_richn_trap)

ggplot(col_spec_richn, aes(y = col_spec_richn,
                           x = locality,
                           fill = trap_type)) +
  geom_bar(stat = "identity",
            position = position_dodge()) +
#  ggtitle(paste0("Kumulativt antall billearter (identifiserte taksa)\\ni hver felletyp per"))
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
  scale_fill_nina(name = "Felletype") +
  ylab("Antall taksa") +
  xlab("Lokalitet")
```

Percentage of catches in each trap type per species

How to make it more readable? Split out all the singletons into a separate graph?

```
col_perc_traptype <- dat %>%
  filter(order == "Coleoptera",
         habitat_type == "Skog") %>%
```

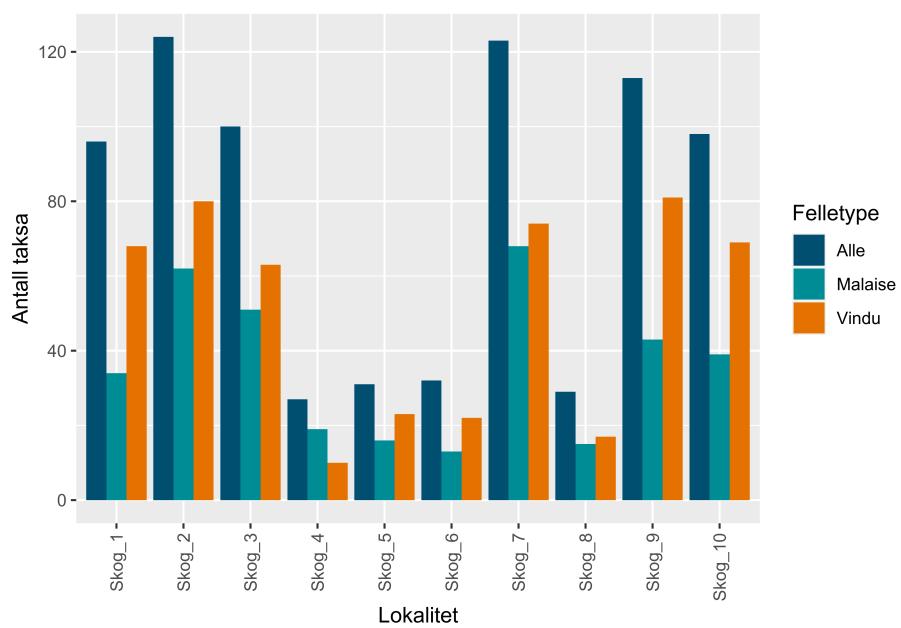


Figure 5: Cumulative number of Coleoptera taxa identified in each trap type

```

group_by(trap_type,
         genus,
         species_latin) %>%
summarize(no_catches = n())

## `summarise()` regrouping output by 'trap_type', 'genus' (override with `groups` argument)
to_plot_temp <- col_perc_tratype %>%
ungroup() %>%
arrange(species_latin,
        trap_type) %>%
filter(no_catches > 1) %>%
group_by(species_latin) %>%
mutate(caught_in = n_distinct(trap_type))

temp_1 <- to_plot_temp %>%
filter(caught_in == 1) %>%
arrange(trap_type, species_latin)

temp_2 <- to_plot_temp %>%
filter(caught_in == 2) %>%
arrange(species_latin, trap_type)

to_plot <- rbind(temp_1, temp_2) %>%
ungroup() %>%
mutate(trap_type = factor(trap_type),
       species_latin = factor(species_latin),
       facet = rep(c(1, 2, 3, 4), times = c(57, 57, 57, 56)))

to_plot %>%
ggplot(.) +
  geom_bar(aes(y = reorder(species_latin, species_latin), x = no_catches, fill = trap_type),
           stat = "identity",
           position = position_dodge()) +
  scale_fill_nina(name = "Trap type") +
  ylab("") +
  xlab("Number of catches") +
  theme(legend.position = "none",
        text = element_text(size=5)) +
  facet_wrap(facets = vars(facet),
             scales = "free_y",
             strip.position = "right",
             ncol = 4)

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

```

```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:  
## returning NA  
  
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```

```

p1 <- to_plot %>%
  slice(1:50) %>%
  group_by(trap_type) %>%
  ggplot(.) +
  geom_bar(aes(y = species_latin, x = no_catches, fill = trap_type),
           stat = "identity",
           position = position_dodge()) +
  scale_fill_nina(name = "Trap type") +
  ylab("") +
  xlab("Number of catches") +
  theme(legend.position = "none",
        text = element_text(size=5))

```

```

p2 <- to_plot %>%
  slice(51:100) %>%
  group_by(trap_type) %>%
  ggplot(.) +
  geom_bar(aes(y = species_latin, x = no_catches, fill = trap_type),
           stat = "identity",
           position = position_dodge()) +
  scale_fill_nina(name = "Trap type") +
  ylab("") +
  xlab("Number of catches") +
  theme(legend.position = "none",
        text = element_text(size=5))

```

```

p3 <- to_plot %>%

```

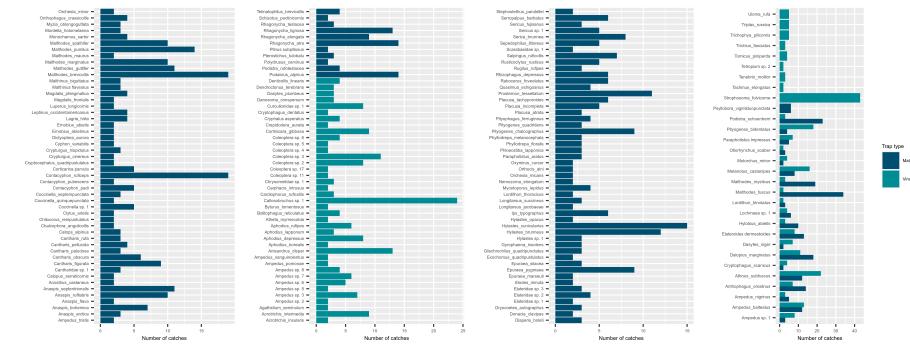
```

    slice(101:150) %>%
  group_by(trap_type) %>%
ggplot(.) +
  geom_bar(aes(y = species_latin, x = no_catches, fill = trap_type),
           stat = "identity",
           position = position_dodge()) +
  scale_fill_nina(name = "Trap type") +
  ylab("") +
  xlab("Number of catches") +
  theme(legend.position = "none",
        text = element_text(size=5))

p4 <- to_plot %>%
  slice(151:200) %>%
  group_by(trap_type) %>%
ggplot(.) +
  geom_bar(aes(y = species_latin, x = no_catches, fill = trap_type),
           stat = "identity",
           position = position_dodge()) +
  scale_fill_nina(name = "Trap type") +
  ylab("") +
  xlab("Number of catches") +
  theme(text = element_text(size=5))

grid.arrange(p1, p2, p3, p4, nrow = 1)

```



```

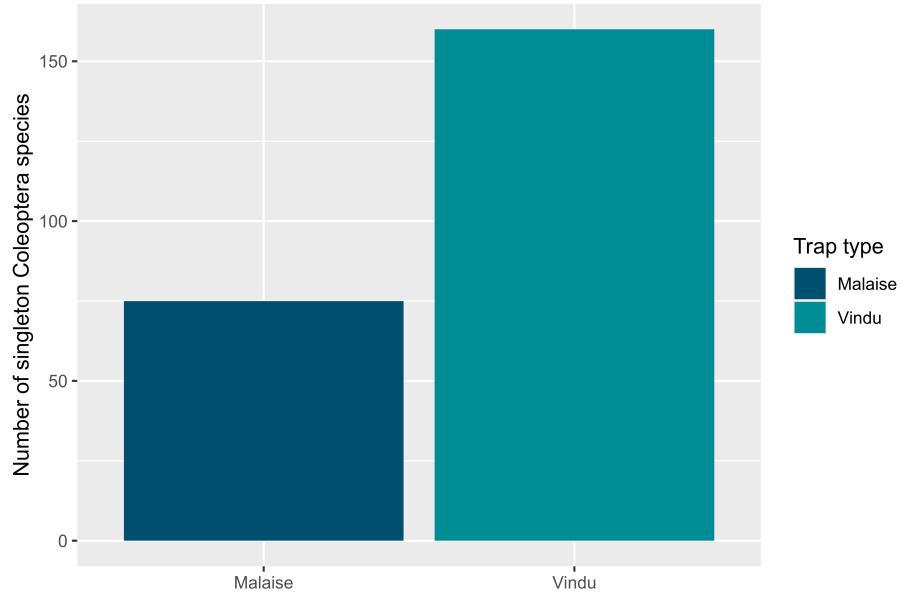
col_perc_tratype %>%
  ungroup() %>%
  arrange(species_latin,
          trap_type) %>%
  filter(no_catches == 1) %>%
  group_by(trap_type) %>%
  summarize(no_singletons = n()) %>%

```

```

ggplot(.) +
  geom_bar(aes(y = no_singletons, x = trap_type, fill = trap_type),
            stat = "identity") +
  scale_fill_nina(name = "Trap type") +
  ylab("Number of singleton Coleoptera species") +
  xlab("")
## `summarise()` ungrouping output (override with `.`groups` argument)

```



Figs to Niclas on Pollinators

Niclas Gyllenstrand asked how efficient the malaisetraps+metabarcoding are at finding pollinators. This could be a relevant graph for the report as well.

```

poll_spec_richn <- dat %>%
  filter(trap_type == "Malaise") %>%
  filter(family == "Andrenidae" |
         family == "Apidae" |
         family == "Colletidae" |
         family == "Halictidae" |
         family == "Megachilidae" |
         family == "Melittidae" |
         family == "Syrphidae" |

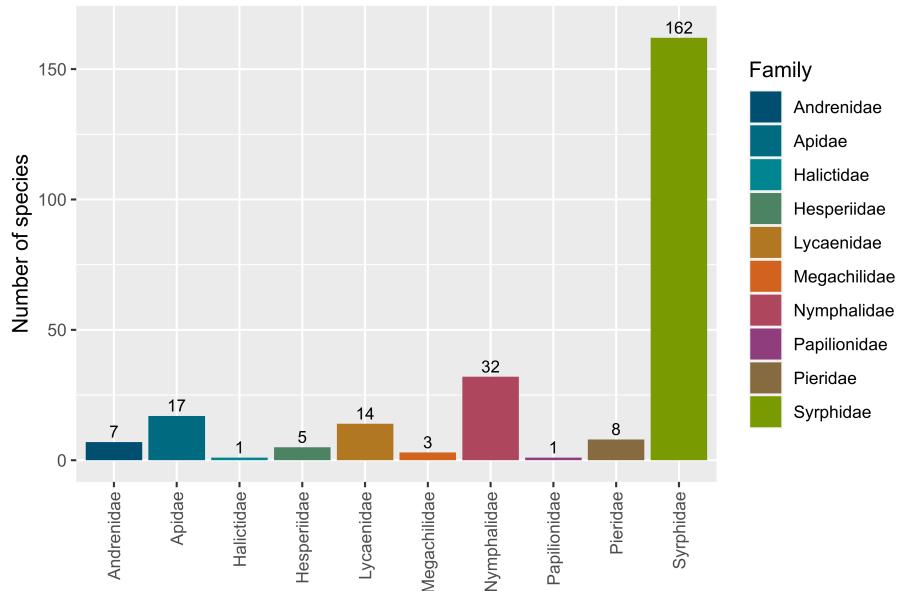
```

```

family == "Hesperiidae" |
family == "Lycaenidae" |
family == "Nymphalidae" |
family == "Papilionidae" |
family == "Pieridae" |
family == "Riodinidae"
) %>%
group_by(family) %>%
distinct(family, genus, species) %>%
summarize(col_spec_richn = n(),
no_unidentified_sp = sum(grepl("sp.", species)))

## `summarise()` ungrouping output (override with `groups` argument)
ggplot(poll_spec_richn, aes(x = family, y = col_spec_richn, label = col_spec_richn)) +
  geom_bar(stat = "identity",
           aes(fill = family)) +
  geom_text(size = 3,
            position = position_nudge(y = 4)) +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
  scale_fill_nina(name = "Family") +
  xlab("") +
  ylab("Number of species")

```



```

pollinator_species <- dat %>%
  filter(trap_type == "Malaise") %>%
  filter(family == "Andrenidae" |
         family == "Apidae" |
         family == "Colletidae" |
         family == "Halictidae" |
         family == "Megachilidae" |
         family == "Melittidae" |
         family == "Syrphidae" |
         family == "Hesperiidae" |
         family == "Lycaenidae" |
         family == "Nymphalidae" |
         family == "Papilionidae" |
         family == "Pieridae" |
         family == "Riodinidae")
    ) %>%
distinct(order, family, genus, species) %>%
arrange(family, genus, species)

dat %>%
  filter(trap_type == "Malaise") %>%
  filter(family == "Apidae") %>%
  distinct(genus, species) %>%
  select(genus, species)

## # A tibble: 17 x 2
##   genus     species
##   <chr>     <chr>
## 1 Apis      mellifera
## 2 Bombus    soroeensis
## 3 Bombus    pascuorum
## 4 Bombus    lucorum
## 5 Bombus    jonellus
## 6 Bombus    pratorum
## 7 Bombus    monticola
## 8 Melipona  illota
## 9 Bombus    consobrinus
## 10 Bombus   cryptarum
## 11 Bombus   sporadicus
## 12 Bombus   cingulatus
## 13 Bombus   hortorum
## 14 Bombus   hypnorum
## 15 Bombus   norvegicus
## 16 Bombus   ashtonii

```

```

## 17 Bombus terrestris
write_csv(pollinator_species,
           path = "out/pollinator_species.csv")

## Warning: The `path` argument of `write_csv()` is deprecated as of readr 1.4.0.
## Please use the `file` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was generated.

```

Phenology graphs

Some “timeseries” throughout the season.

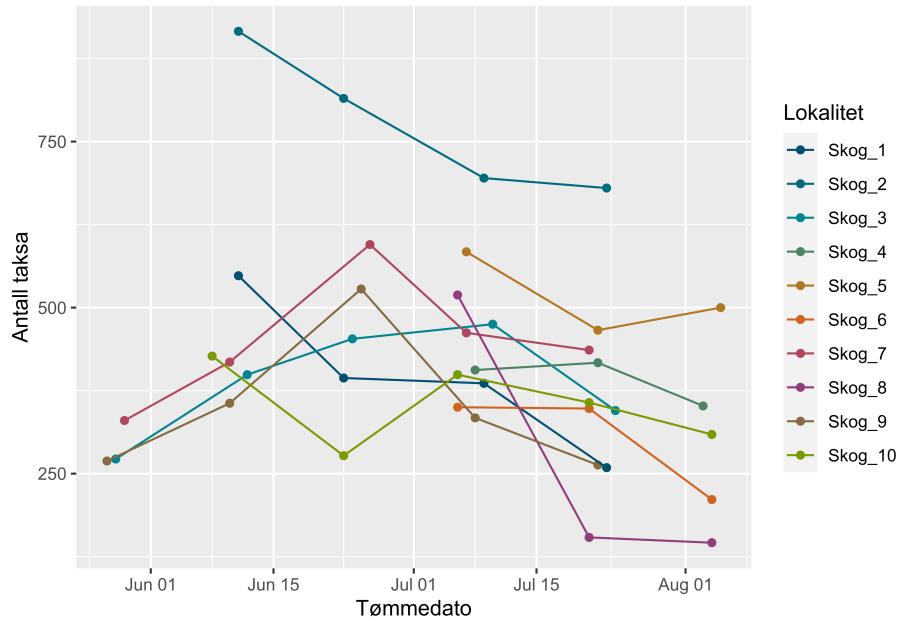
```

seasonAvgNo <- dat %>%
  filter(weeks_sampled == 2) %>%
  group_by(habitat_type, dateemptied, locality) %>%
  summarise(no_species = n_distinct(genus, species),
            sum_biomass = sum(Vekt_flaske_.insekter_vaat_.g., na.rm = T) / no_species)

## `summarise()` regrouping output by 'habitat_type', 'dateemptied' (override with `groups`)
# test <- seasonAvgNo <- dat %>%
#   filter(weeks_sampled == 2) %>%
#   group_by(habitat_type, dateemptied, locality) %>%
#   select(habitat_type, dateemptied, locality, Vekt_flaske_.insekter_vaat_.g.) %>%
#   distinct() %>%
#   summarise(sum(Vekt_flaske_.insekter_vaat_.g., na.rm = T))

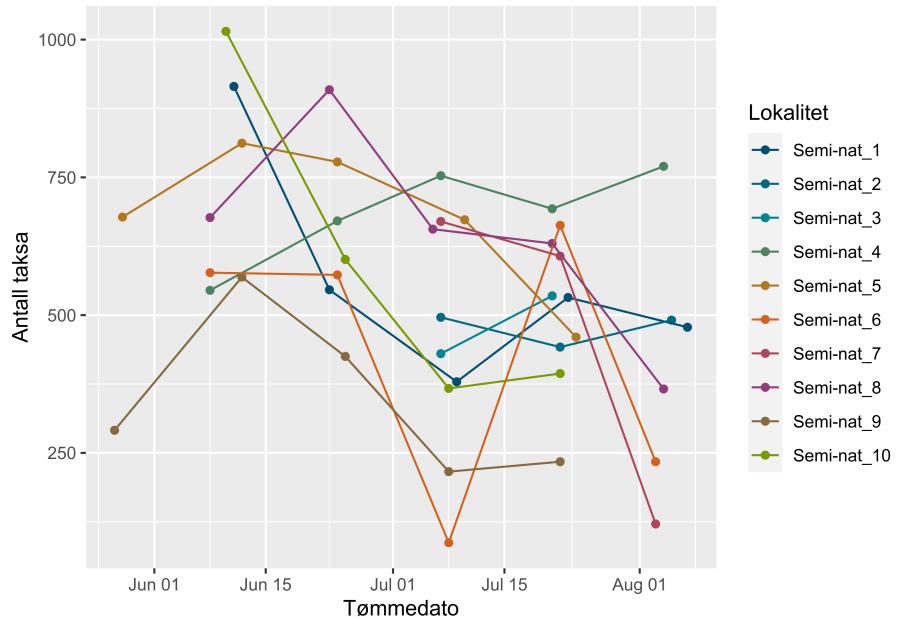
seasonAvgNo %>%
  filter(habitat_type == "Skog") %>%
  ggplot() +
  geom_point(aes(x = dateemptied, y = no_species, color = locality)) +
  geom_line(aes(x = dateemptied, y = no_species, color = locality)) +
  ylab("Antall taksa") +
  xlab("Tømmedato") +
  scale_color_nina(name = "Lokalitet")

```

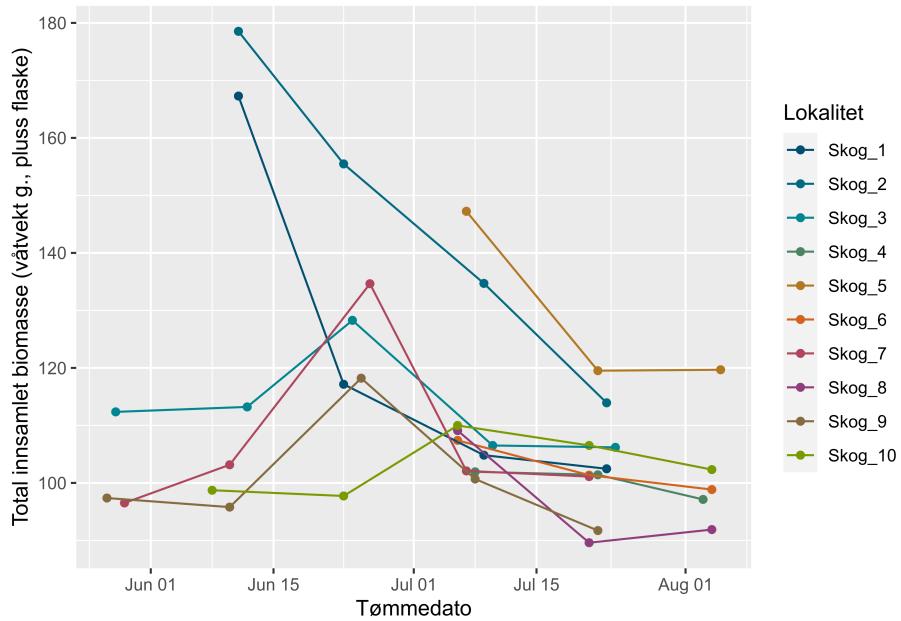


```

seasonAvgNo %>%
  filter(habitat_type == "SN_Gressmark") %>%
  ggplot() +
  geom_point(aes(x = dateemptied, y = no_species, color = locality)) +
  geom_line(aes(x = dateemptied, y = no_species, color = locality)) +
  ylab("Antall taksa") +
  xlab("Tømmedato") +
  scale_color_nina(name = "Lokalitet")
  
```

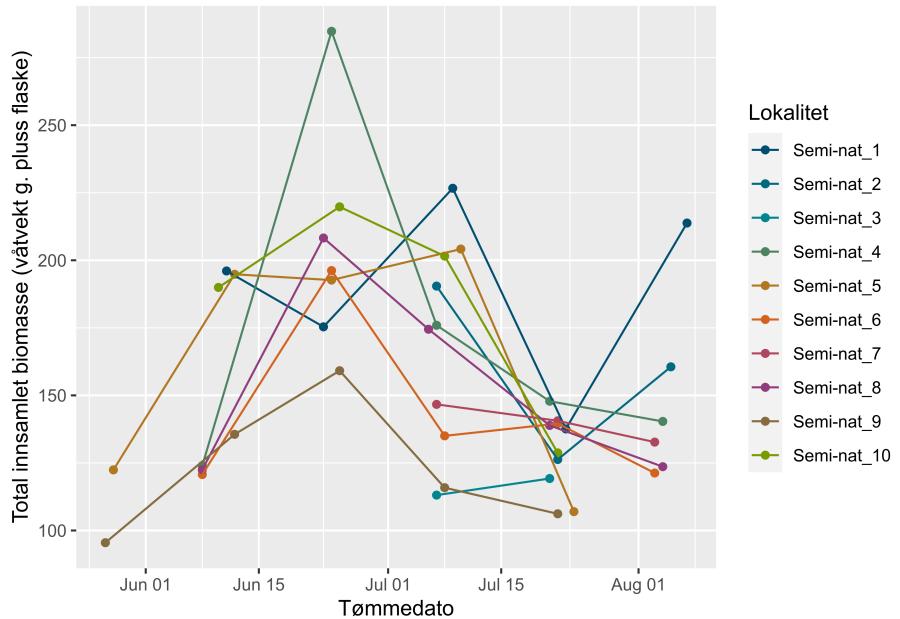


```
seasonAvgNo %>%
  filter(habitat_type == "Skog") %>%
  ggplot() +
  geom_point(aes(x = dateemptied, y = sum_biomass, color = locality)) +
  geom_line(aes(x = dateemptied, y = sum_biomass, color = locality)) +
  ylab("Total innsamlet biomasse (våtvekt g., pluss flaske)") +
  xlab("Tømmedato") +
  scale_color_nina(name = "Lokalitet")
```



```

seasonAvgNo %>%
  filter(habitat_type == "SN_Gressmark") %>%
  ggplot() +
  geom_point(aes(x = dateemptied, y = sum_biomass, color = locality)) +
  geom_line(aes(x = dateemptied, y = sum_biomass, color = locality)) +
  ylab("Total innsamlet biomasse (våtvekt g. pluss flaske)") +
  xlab("Tømmedato") +
  scale_color_nina(name = "Lokalitet")
  
```



Plot some weather data

```
logger_tbl <- tbl(con,
                   in_schema("loggers", "logger_data")) %>%
  select(-id)

logger_dep_tbl <- tbl(con,
                      in_schema("loggers", "logger_deployments")) %>%
  select(-id)

logger_data <- logger_tbl %>%
  left_join(logger_dep_tbl,
            by = c("logger_id" = "logger_id",
                  "logger_type" = "logger_type")) %>%
  mutate(day = as.Date(date))
```

Plot average values for each site during July

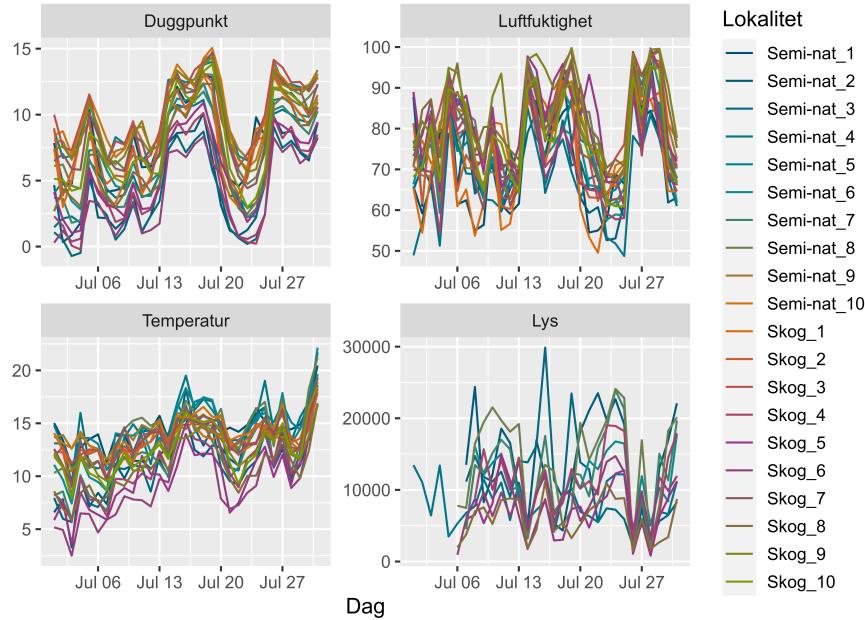
```
tt <- logger_data %>%
  group_by(location, day, data_type) %>%
  summarize(value = mean(value)) %>%
  filter(day >= '2020-07-01' &
         day < '2020-08-01'
```

```

) %>%
collect() %>%
mutate(Lokalitet = factor(location, levels = c(paste0("Semi-nat_", 1:10), paste0("Skog_", 1:10)),
                           mutate(data_type = factor(data_type, levels = )))
##Why can't I set the levels in the pipe?
levels(tt$data_type) <- c("Duggpunkt", "Luftfuktighet", "Temperatur", "Lys")

tt %>%
  ggplot(.) +
  geom_line(aes(x = day, y = value, color = Lokalitet)) +
  facet_wrap(~data_type,
             scales = "free") +
  scale_color_nina(name = "Lokalitet") +
  xlab("Dag") +
  ylab("") +
  theme(legend.key.height = unit(0.5, "cm"))

```



Sampling time analysis

Time to look at the impact of sampling time, 2 vs 4 weeks.

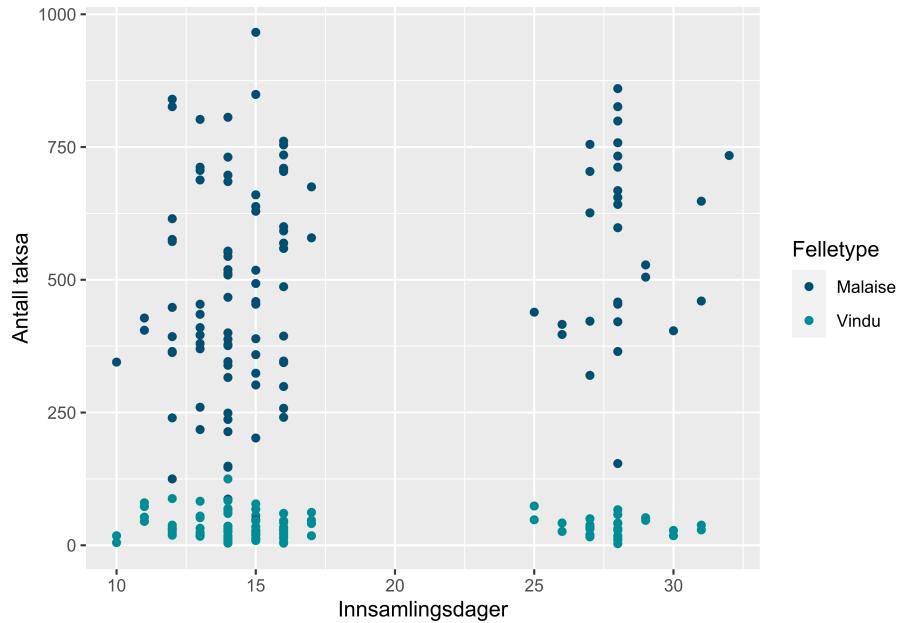
First off, simple plot of species richness against days sampled.

```

dat %>%
  group_by(locality,
           trap,
           trap_type,
           empty_week,
           weeks_sampled,
           days_collected) %>%
  summarise(no_spec = n_distinct(order, family, genus, species)) %>%
  ggplot(aes(x = days_collected, y = no_spec)) +
  geom_point(aes(color = trap_type)) +
  scale_color_nina(name = "Felletype") +
  ylab("Antall taksa") +
  xlab("Innsamlingsdager")

```

`summarise()` regrouping output by 'locality', 'trap', 'trap_type', 'empty_week', 'weeks_sampled'



Not easy to see any patterns here, since there is such variation in the catches throughout the season. We need to sum up the catches in the 2 2-week periods and compare to the single 4 week periods.

We first identify which of the 2-week samples that should be aggregated.

```

#4-week "target" to agg to
week_4 <- dat %>%
  filter(weeks_sampled == 4) %>%
  select(locality,

```

```

            empty_week) %>%
distinct() %>%
mutate(agg_id = 1:n())

#add 2 weeks earlier
earlier_2_weeks <- week_4 %>%
  select(locality,
         agg_id) %>%
  mutate(empty_week = week_4$empty_week - 2)

which_to_agg <- week_4 %>%
  bind_rows(earlier_2_weeks)

#add aggregation ids to 2-week samplings
to_agg <- dat %>%
  filter(weeks_sampled == 2) %>%
  left_join(which_to_agg,
            by = c("locality" = "locality",
                  "empty_week" = "empty_week"))

```

Check which didn't get an aggregation

```

to_agg %>%
  filter(is.na(agg_id)) %>%
  select(locality,
         empty_week,
         trap) %>%
distinct() %>%
arrange(empty_week,
        locality) %>%
print(n = Inf)

## # A tibble: 46 x 3
##   locality   empty_week trap
##   <fct>       <dbl> <chr>
## 1 Semi-nat_1      24 MF1
## 2 Semi-nat_1      24 MF2
## 3 Semi-nat_10     24 MF1
## 4 Semi-nat_10     24 MF2
## 5 Skog_1          24 MF1
## 6 Skog_1          24 MF2
## 7 Skog_1          24 VF1
## 8 Skog_1          24 VF2
## 9 Skog_1          24 VF3
## 10 Skog_1         24 VF4
## 11 Skog_2          24 MF1

```

```

## 12 Skog_2          24 MF2
## 13 Skog_2          24 VF1
## 14 Skog_2          24 VF2
## 15 Skog_2          24 VF3
## 16 Skog_2          24 VF4
## 17 Semi-nat_1      30 MF1
## 18 Semi-nat_5      30 MF1
## 19 Semi-nat_9      30 MF1
## 20 Semi-nat_10     30 MF1
## 21 Skog_1          30 MF1
## 22 Skog_1          30 VF1
## 23 Skog_1          30 VF3
## 24 Skog_2          30 MF1
## 25 Skog_2          30 VF1
## 26 Skog_2          30 VF3
## 27 Skog_3          30 MF1
## 28 Skog_3          30 VF1
## 29 Skog_3          30 VF3
## 30 Skog_7          30 MF1
## 31 Skog_7          30 VF1
## 32 Skog_7          30 VF3
## 33 Skog_9          30 MF1
## 34 Skog_9          30 VF1
## 35 Skog_9          30 VF3
## 36 Semi-nat_1      32 MF1
## 37 Semi-nat_2      32 MF1
## 38 Semi-nat_4      32 MF1
## 39 Semi-nat_6      32 MF1
## 40 Semi-nat_7      32 MF1
## 41 Semi-nat_8      32 MF1
## 42 Skog_4          32 MF1
## 43 Skog_5          32 MF1
## 44 Skog_6          32 MF1
## 45 Skog_8          32 MF1
## 46 Skog_10         32 MF1

```

The samples from week 24 are expected, since not all traps where set up early enough to get 2 emptyings by then.

```

dat %>%
  filter(locality == 'Semi-nat_2' &
         empty_week == 34) %>%
  select(locality,
         empty_week,
         dateemptied,
         weeks_sampled,

```

```

    trap,
    GenlabID) %>%
distinct()

## # A tibble: 0 x 6
## # ... with 6 variables: locality <fct>, empty_week <dbl>, dateemptied <date>,
## #   weeks_sampled <dbl>, trap <chr>, GenlabID <chr>

But Semi-nat_1, week_32, trap MF2 should be there. Semi-nat_5 as well.
Seems that these haven't been run yet. I'll remove these for the comparison.

#Sum the genetic reads to combine the two weeks
agg_data_2_week <- to_agg %>%
  filter(!is.na(agg_id)) %>%
  group_by(locality,
           trap_type,
           trap,
           agg_id,
           species_latin) %>%
  summarise(value = sum(value)) %>%
  ungroup()

## `summarise()` regrouping output by 'locality', 'trap_type', 'trap', 'agg_id' (override w
#Add the week information for the second sampling
agg_data_2_week <- agg_data_2_week %>%
  left_join(week_4,
            by = c("agg_id" = "agg_id",
                  "locality" = "locality")) %>%
  mutate(weeks_sampled = 2) %>%
  select(locality,
         empty_week,
         weeks_sampled,
         trap_type,
         trap,
         species_latin,
         value)

#Select only the original 4 week samplings
data_4_week <- dat %>%
  filter(weeks_sampled == 4) %>%
  select(locality,
         empty_week,
         weeks_sampled,
         trap_type,
         trap,

```

```

    species_latin,
    value)

#Add the original 4 weeks to the summarized 2 2-week samplings
week_comp_data <- agg_data_2_week %>%
  bind_rows(data_4_week)

```

Summarise the number of species in both sample lengths.

```

no_species_weeks <- week_comp_data %>%
  group_by(locality,
           empty_week,
           weeks_sampled,
           trap_type) %>%
  summarise(no_species = n())

## `summarise()` regrouping output by 'locality', 'empty_week', 'weeks_sampled' (override with `.`groups` argument)
#Check comparison
no_species_weeks %>%
  group_by(locality,
           empty_week,
           trap_type) %>%
  summarise(no_comp = n()) %>%
  print(n = Inf)

## `summarise()` regrouping output by 'locality', 'empty_week' (override with `.`groups` argument)
## # A tibble: 43 x 4
##   locality   empty_week trap_type no_comp
##   <fct>       <dbl> <chr>     <int>
## 1 Semi-nat_1      28 Malaise     2
## 2 Semi-nat_2      30 Malaise     2
## 3 Semi-nat_3      30 Malaise     2
## 4 Semi-nat_4      26 Malaise     2
## 5 Semi-nat_4      30 Malaise     2
## 6 Semi-nat_5      24 Malaise     2
## 7 Semi-nat_5      28 Malaise     2
## 8 Semi-nat_6      26 Malaise     2
## 9 Semi-nat_6      30 Malaise     2
## 10 Semi-nat_7     30 Malaise     2
## 11 Semi-nat_8     26 Malaise     2
## 12 Semi-nat_8     30 Malaise     2
## 13 Semi-nat_9     24 Malaise     2
## 14 Semi-nat_9     28 Malaise     2
## 15 Semi-nat_10    28 Malaise     2

```

```

## 16 Skog_1          28 Malaise    2
## 17 Skog_1          28 Vindu      2
## 18 Skog_2          28 Malaise    2
## 19 Skog_2          28 Vindu      2
## 20 Skog_3          24 Malaise    2
## 21 Skog_3          24 Vindu      2
## 22 Skog_3          28 Malaise    2
## 23 Skog_3          28 Vindu      2
## 24 Skog_4          30 Malaise    2
## 25 Skog_4          30 Vindu      2
## 26 Skog_5          30 Malaise    2
## 27 Skog_5          30 Vindu      2
## 28 Skog_6          30 Malaise    2
## 29 Skog_6          30 Vindu      2
## 30 Skog_7          24 Malaise    2
## 31 Skog_7          24 Vindu      2
## 32 Skog_7          28 Malaise    2
## 33 Skog_7          28 Vindu      2
## 34 Skog_8          30 Malaise    2
## 35 Skog_8          30 Vindu      2
## 36 Skog_9          24 Malaise    2
## 37 Skog_9          24 Vindu      2
## 38 Skog_9          28 Malaise    2
## 39 Skog_9          28 Vindu      2
## 40 Skog_10         26 Malaise    2
## 41 Skog_10         26 Vindu      2
## 42 Skog_10         30 Malaise    2
## 43 Skog_10         30 Vindu      2

```

Make a comparison table.

```

comp_species_week <- no_species_weeks %>%
  pivot_wider(id_cols = c(locality,
                           empty_week,
                           trap_type),
              names_from = weeks_sampled,
              values_from = no_species,
              names_prefix = "sample_time_") %>%
  mutate(diff_sample_time = sample_time_4 - sample_time_2,
        prc_diff_sample_time = (sample_time_4 - sample_time_2) / sample_time_2)

```

Quality check of a few rows. Seems OK.

```

dat %>%
  filter(locality == "Semi-nat_1" &
         (empty_week == 26 | empty_week == 28) &
         trap == "MF1")

```

```

    ) %>%
summarize(no_spec = n_distinct(species_latin))

## # A tibble: 1 x 1
##   no_spec
##       <int>
## 1      776

dat %>%
  filter(locality == "Semi-nat_5" &
        (empty_week == 22 | empty_week == 24) &
        trap == "MF1"
    ) %>%
  summarize(no_spec = n_distinct(species_latin))

## # A tibble: 1 x 1
##   no_spec
##       <int>
## 1      1219

dat %>%
  filter(locality == "Semi-nat_5" &
        (empty_week == 24) &
        trap == "MF2"
    ) %>%
  summarize(no_spec = n_distinct(species_latin))

## # A tibble: 1 x 1
##   no_spec
##       <int>
## 1      648

dat %>%
  filter(locality == "Semi-nat_6" &
        (empty_week == 26) &
        trap == "MF2"
    ) %>%
  summarize(no_spec = n_distinct(species_latin))

## # A tibble: 1 x 1
##   no_spec
##       <int>
## 1      826

week_comp_data %>%
  filter(locality == "Semi-nat_5" &
        (empty_week == 24) &
        trap == "MF2"
    )

```

```

    ) %>%
summarize(no_spec = n_distinct(species_latin))

## # A tibble: 1 x 1
##   no_spec
##     <int>
## 1      648

no_species_weeks %>%
  filter(locality == "Semi-nat_5" &
        empty_week == 24)

## # A tibble: 2 x 5
## Groups:   locality, empty_week, weeks_sampled [2]
##   locality   empty_week weeks_sampled trap_type no_species
##   <fct>          <dbl>       <dbl> <chr>        <int>
## 1 Semi-nat_5      24           2 Malaise      1219
## 2 Semi-nat_5      24           4 Malaise      648

comp_species_week %>%
  group_by(locality) %>%
  filter(trap_type == "Malaise") %>%
  ggplot(.) +
  geom_point(aes(x = empty_week, y = diff_sample_time, color = locality)) +
  geom_line(aes(x = empty_week, y = diff_sample_time, color = locality)) +
  scale_color_nina(name = "Lokalitet") +
  ylab("Diff. kumulativ 2 uker - 4 uker (no. taksa)") +
  xlab("Tømmingsuke, 4 ukerstømming") +
  geom_hline(yintercept = 0) +
  theme(legend.key.height = unit(0.5, "cm"))

comp_species_week %>%
  group_by(locality) %>%
  filter(trap_type == "Malaise") %>%
  ggplot(.) +
  geom_point(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  geom_line(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  scale_color_nina(name = "Lokalitet") +
  ylab("% Diff. kumulativ 2 uker - 4 uker") +
  xlab("Tømmingsuke, 4 ukerstømming") +
  geom_hline(yintercept = 0) +
  theme(legend.key.height = unit(0.5, "cm"))

comp_species_week %>%
  group_by(locality) %>%
  filter(trap_type == "Vindu") %>%
  ggplot(.) +

```

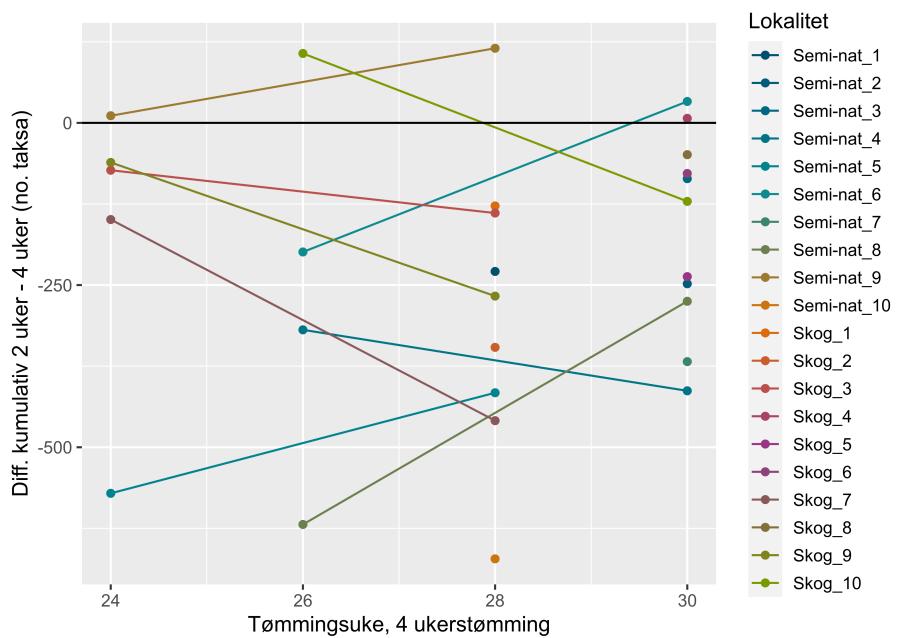


Figure 6: Difference (g.) in cumulative species richness over 2 2-week samplings, compared to 1 4 week sampling. Catch in 1 Malaise trap per period. Negative values indicate that 4-week samplings gave lower insect species richness than the two 2-week samplings.

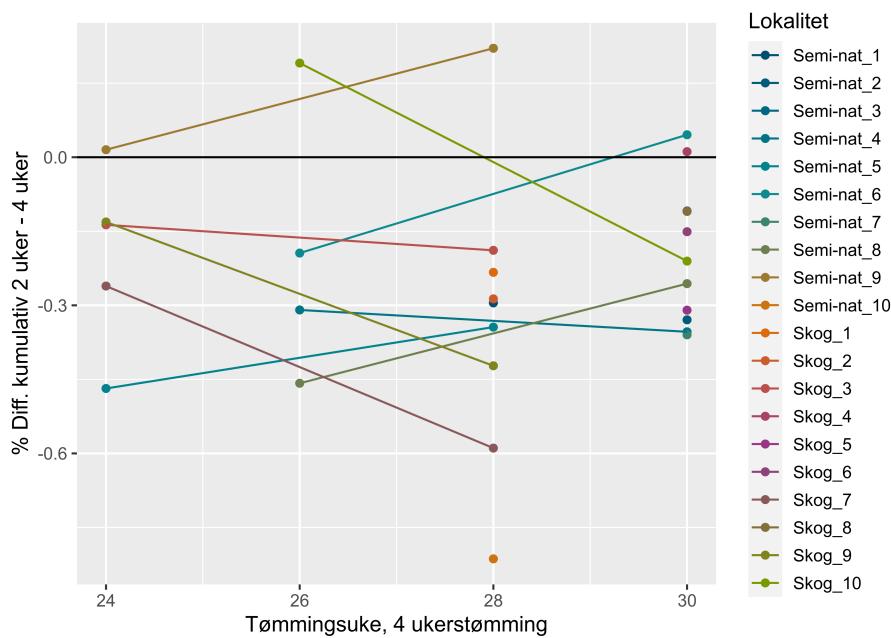


Figure 7: Percentage difference in cumulative species richness over 2 2-week samplings, compared to 1 4 week sampling. Catch in 1 Malaise trap per period. Negative values indicate that 4-week samplings gave lower insect species richness than the two 2-week samplings.

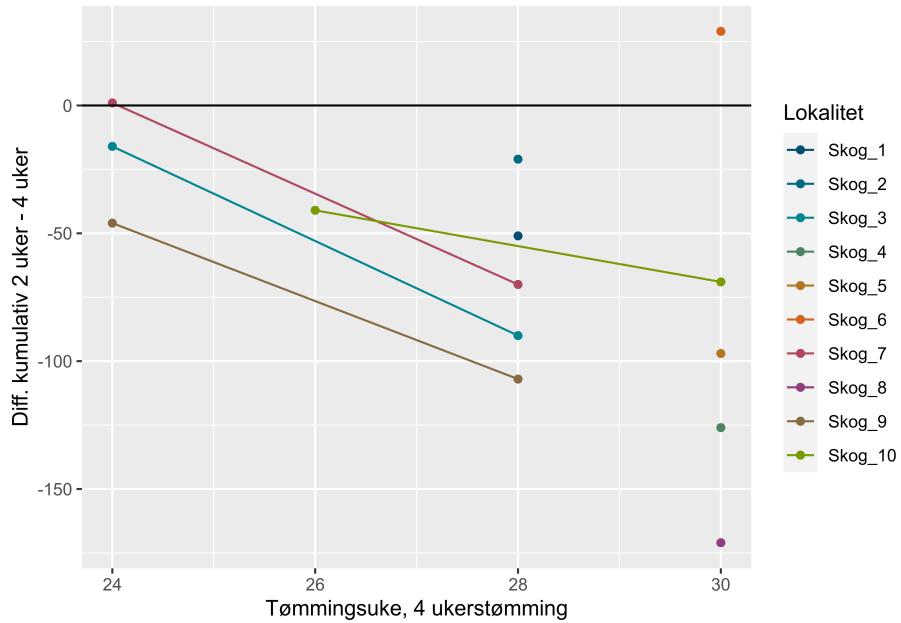


Figure 8: Difference in cumulative species richness over 2 2-week samplings, compared to 1 4 week sampling. Catch in 1 Malaise trap per period. Negative values indicate that 4-week samplings gave lower insect species richness than the two 2-week samplings.

```

geom_point(aes(x = empty_week, y = diff_sample_time, color = locality)) +
  geom_line(aes(x = empty_week, y = diff_sample_time, color = locality)) +
  scale_color_nina(name = "Lokalitet") +
  ylab("Diff. kumulativ 2 uker - 4 uker") +
  xlab("Tømmingsuke, 4 ukerstømning") +
  geom_hline(yintercept = 0)

comp_species_week %>%
  group_by(locality) %>%
  filter(trap_type == "Vindu") %>%
  ggplot(.) +
  geom_point(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  geom_line(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  scale_color_nina(name = "Lokalitet") +
  ylab("% Diff. kumulativ 2 uker - 4 uker") +
  xlab("Tømmingsuke, 4 ukerstømning") +
  geom_hline(yintercept = 0)

```

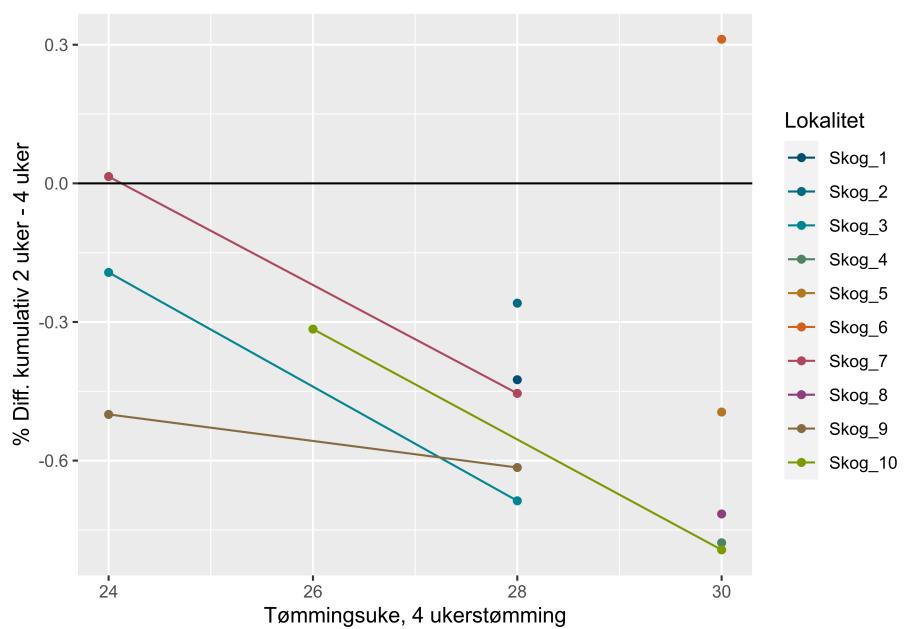


Figure 9: Percentage difference in cumulative species richness over 2 2-week samplings, compared to 1 4 week sampling. Catch in 2 window traps per period. Negative values indicate that 4-week samplings gave lower insect species richness than the two 2-week samplings.

A similar comparison, but for biomass.

```
biomass_agg_data_2_week <- to_agg %>%
  filter(!is.na(agg_id)) %>%
  select(locality,
         empty_week,
         trap_type,
         trap,
         agg_id,
         biomass = Toerrvekt_.g.) %>%
  distinct() %>%
  arrange(locality,
          empty_week,
          trap) %>%
  group_by(locality,
           trap_type,
           agg_id) %>%
  summarise(empty_week = max(empty_week),
            biomass = sum(biomass)
            ) %>%
  ungroup() %>%
  select(-agg_id)

## `summarise()` regrouping output by 'locality', 'trap_type' (override with `.`.groups` argument)
biomass_data_4_week <- dat %>%
  filter(weeks_sampled == 4) %>%
  select(locality,
         empty_week,
         trap_type,
         trap,
         biomass = Toerrvekt_.g.) %>%
  distinct() %>%
  arrange(locality,
          empty_week,
          trap) %>%
  group_by(locality,
           empty_week,
           trap_type) %>%
  summarise(empty_week = max(empty_week),
            biomass = sum(biomass)
            ) %>%
  ungroup()

## `summarise()` regrouping output by 'locality', 'empty_week' (override with `.`.groups` argument)
```

```

#Make comparison table
biomass_comp <- biomass_agg_data_2_week %>%
  left_join(biomass_data_4_week,
            by = c("locality" = "locality",
                  "empty_week" = "empty_week",
                  "trap_type" = "trap_type"),
            suffix = c("_2_weeks", "_4_weeks")) %>%
  mutate(diff_sample_time = biomass_4_weeks - biomass_2_weeks,
         prc_diff_sample_time = (biomass_4_weeks - biomass_2_weeks) / biomass_2_weeks)

biomass_comp %>%
  group_by(locality) %>%
  filter(trap_type == "Malaise") %>%
  ggplot(.) +
  geom_point(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  geom_line(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  scale_color_nina(name = "Lokalitet") +
  ylab("% Diff. kumulativ 2 uker - 4 uker") +
  xlab("Tømmingsuke, 4 ukerstømming") +
  geom_hline(yintercept = 0) +
  theme(legend.key.height = unit(0.5, "cm"))

## Warning: Removed 3 rows containing missing values (geom_point).
## Warning: Removed 3 row(s) containing missing values (geom_path).

We can do the same comparison with wet weight, although we might expect
that this will add some weight of the ethanol and the bottles, which will lead
to bias when we sum these together for the 2 weeks. Anyway, this is the way it
looks for wet weight.

biomass_agg_data_2_week <- to_agg %>%
  filter(!is.na(agg_id)) %>%
  select(locality,
         empty_week,
         trap_type,
         trap,
         agg_id,
         biomass = Vaatvekt_.g.) %>%
  distinct() %>%
  arrange(locality,
          empty_week,
          trap) %>%
  group_by(locality,
           trap_type,
           agg_id) %>%
  summarise(empty_week = max(empty_week),
           

```

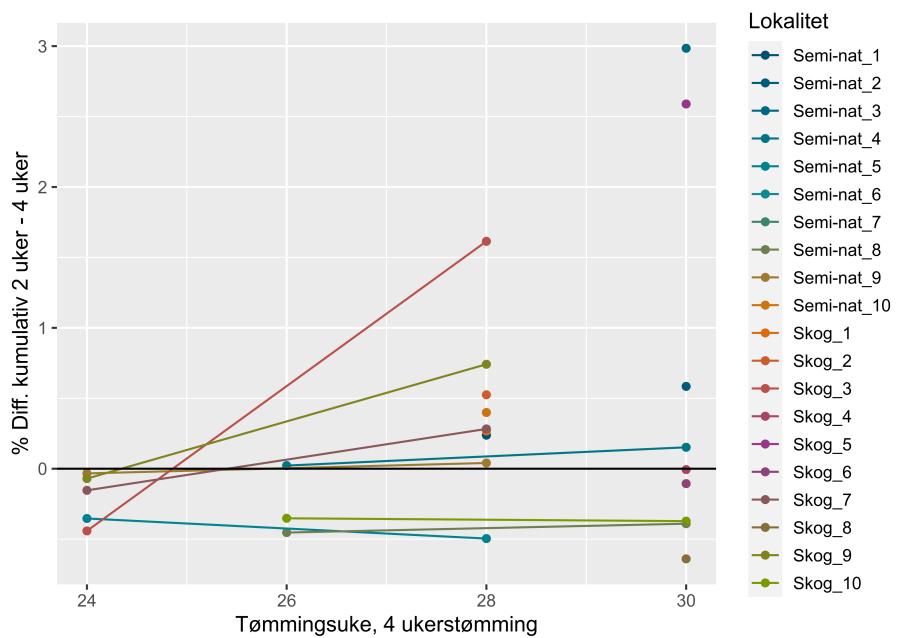


Figure 10: Percentage difference in cumulative dry weight over 2 2-week samplings, compared to 1 4 week sampling. Catch in 1 Malaise trap per period. Negative values indicate that 4-week samplings gave lower insect species richness than the two 2-week samplings.

```

        biomass = sum(biomass)
    ) %>%
ungroup() %>%
select(-agg_id)

## `summarise()` regrouping output by 'locality', 'trap_type' (override with `.`groups` argument)
biomass_data_4_week <- dat %>%
  filter(weeks_sampled == 4) %>%
  select(locality,
         empty_week,
         trap_type,
         trap,
         biomass = Vaatvekt_.g.) %>%
distinct() %>%
arrange(locality,
        empty_week,
        trap) %>%
group_by(locality,
          empty_week,
          trap_type) %>%
summarise(empty_week = max(empty_week),
          biomass = sum(biomass)
    ) %>%
ungroup()

## `summarise()` regrouping output by 'locality', 'empty_week' (override with `.`groups` argument)
#Make comparison table
biomass_comp <- biomass_agg_data_2_week %>%
  left_join(biomass_data_4_week,
            by = c("locality" = "locality",
                  "empty_week" = "empty_week",
                  "trap_type" = "trap_type"),
            suffix = c("_2_weeks", "_4_weeks")) %>%
  mutate(diff_sample_time = biomass_2_weeks - biomass_4_weeks,
         prc_diff_sample_time = (biomass_2_weeks - biomass_4_weeks) / biomass_2_weeks)

biomass_comp %>%
  group_by(locality) %>%
  filter(trap_type == "Malaise") %>%
  ggplot(.) +
  geom_point(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  geom_line(aes(x = empty_week, y = prc_diff_sample_time, color = locality)) +
  scale_color_nina(name = "Lokalitet") +
  ylab("% Diff. kumulativ 2 uker - 4 uker") +
  xlab("Tømmingsuke, 4 ukerstømming") +

```

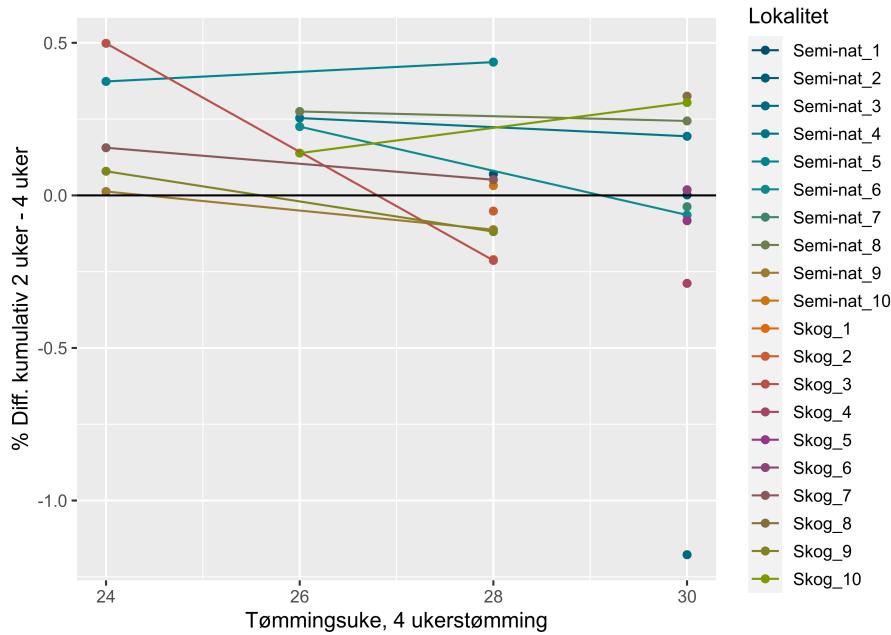


Figure 11: Percentage difference in cumulative wet weight over 2 2-week samplings, compared to 1 4 week sampling. Catch in 1 Malaise trap per period. Negative values indicate that 4-week samplings gave lower insect species richness than the two 2-week samplings.

```
geom_hline(yintercept = 0) +
  theme(legend.key.height = unit(0.5, "cm"))
```

Compare the ethanol to the propglykol window traps

```
liquid_comp <- dat %>%
  filter(trap_type == "Vindu") %>%
  group_by(locality,
    trap,
    liquid,
    weeks_sampled,
    empty_week,
    sample_id
  ) %>%
  summarise(no_species = n_distinct(species_latin))
```

```

## `summarise()` regrouping output by 'locality', 'trap', 'liquid', 'weeks_sampled', 'empty_week'
liquid_comp

## # A tibble: 101 x 7
## # Groups: locality, trap, liquid, weeks_sampled, empty_week [101]
##   locality trap liquid    weeks_sampled empty_week sample_id no_species
##   <fct>    <chr>  <chr>        <dbl>      <dbl> <chr>       <int>
## 1 Skog_1   VF1   Ethanol        2          24 skog_1_VF1_we~     43
## 2 Skog_1   VF1   Ethanol        2          26 skog_1_VF1_we~     31
## 3 Skog_1   VF1   Ethanol        2          28 skog_1_VF1_we~     30
## 4 Skog_1   VF1   Ethanol        2          30 skog_1_VF1_we~     27
## 5 Skog_1   VF2   Ethanol        2          24 skog_1_VF2_we~     60
## 6 Skog_1   VF2   Ethanol        4          28 skog_1_VF2_we~     28
## 7 Skog_1   VF3   PropGl_Eth~        2          24 skog_1_VF3_we~     46
## 8 Skog_1   VF3   PropGl_Eth~        2          26 skog_1_VF3_we~     31
## 9 Skog_1   VF3   PropGl_Eth~        2          28 skog_1_VF3_we~     46
## 10 Skog_1  VF3   PropGl_Eth~       2          30 skog_1_VF3_we~     18
## # ... with 91 more rows

liquid_mod_0 <- glmer(no_species ~ liquid * weeks_sampled + (1|empty_week) + (1 | locality),
                       family = "poisson",
                       data = liquid_comp)

isSingular(liquid_mod_0)

## [1] FALSE
summary(liquid_mod_0)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: no_species ~ liquid * weeks_sampled + (1 | empty_week) + (1 |
##           locality)
## Data: liquid_comp
##
##      AIC      BIC  logLik deviance df.resid
## 1620.7  1636.4 -804.4   1608.7      95
##
## Scaled residuals:
##      Min      1Q  Median      3Q     Max
## -5.8003 -2.5318 -0.8503  2.0783 10.6207
##
## Random effects:
## Groups      Name        Variance Std.Dev.

```

```

##  locality  (Intercept) 0.08466  0.2910
##  empty_week (Intercept) 0.05510  0.2347
## Number of obs: 101, groups: locality, 10; empty_week, 5
##
## Fixed effects:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  3.62137   0.15886  22.797 <2e-16 ***
## liquidPropGl_Ethanol        -0.03270   0.10194  -0.321  0.748
## weeks_sampled                -0.04275   0.02861  -1.494  0.135
## liquidPropGl_Ethanol:weeks_sampled 0.04058   0.03826   1.061  0.289
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) lqPG_E wks_sm
## lqdPrpGl_Et -0.342
## weeks_smpld -0.438  0.679
## lqdPrpG_E:_  0.328 -0.944 -0.728

```

I struggle to model this with all the random effect I would like. I'm not able to include a id level random effect to account for overdispersion for example. Anyway, the results give an indication of the differences in the data.

```

liquid_pred <- ggpredict(liquid_mod_0,
                           terms = c("liquid", "weeks_sampled"))

plot(liquid_pred) +
  scale_color_nina(name = "Antall uker") +
  ggtitle("") +
  ylab("Antall taksa") +
  xlab("Væske i vindusfelle")

## Scale for 'colour' is already present. Adding another scale for 'colour',
## which will replace the existing scale.

```

Ano-registations

Here is some simple graphs of the ANO measurements at the locations. IKKE KLAR, gjør bedre fargeskala

```

ano_arter <- tbl(con,
                   in_schema("ano", "herb_species"))

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:

```

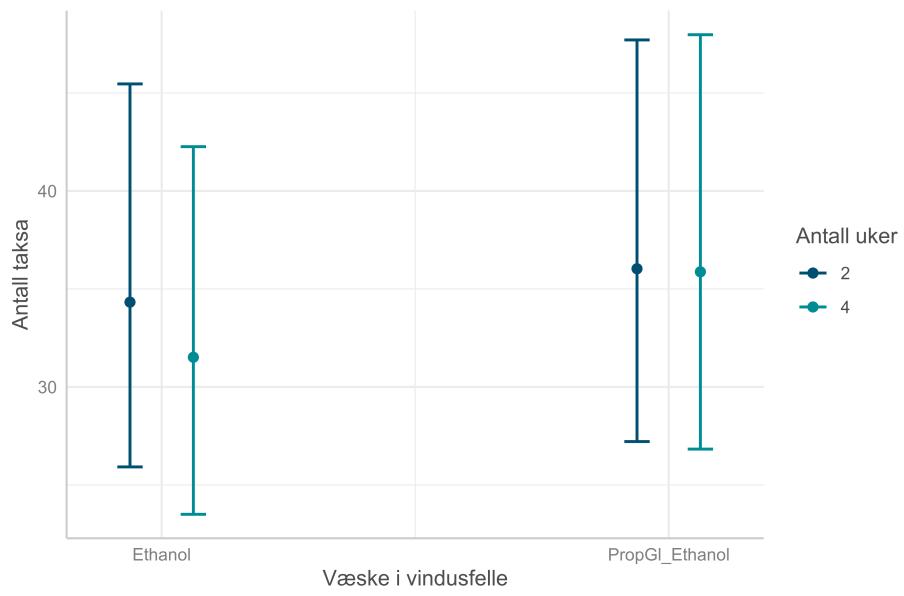


Figure 12: Modelled difference in number of taxa found in window traps, in 2/4 weeks sampling and ethanol/propylen-glycole liquid.

```

## (unrecognized PostgreSQL field type uuid (id:2950) in column 1)
ano_plots <- tbl(con,
                     in_schema("ano", "survey_points"))

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type geometry (id:14917875) in column 56)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type geometry (id:14917875) in column 57)
trap_loc <- tbl(con,
                     in_schema("traps", "locations"))

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)
trap_loc %>%
  left_join(ano_plots,
              by = c("ano_flate_id" = "ano_flate_id")) %>%
  select(-c(geom_punched, geom_inferred)) %>%
  collect() %>%
  select(location, ano_flate_id, global_id) %>%
  distinct() %>%
  print(n = Inf)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 4)

## # A tibble: 170 x 3
##   location    ano_flate_id global_id
##   <chr>        <chr>       <chr>
## 1 Semi-nat_1  AN02090     8f1e3337-2266-a776-2ec4-fe1a20f07a91
## 2 Semi-nat_2  AN04425     b2720789-9d0b-5c40-5ca5-f864591c3d5d
## 3 Semi-nat_3  AN03017     dc774f76-2002-3861-4017-cd66781e422c
## 4 Semi-nat_4  AN04145     a823bb2b-610e-35be-7ff3-bd9e263e6a31
## 5 Semi-nat_5  AN02860     5f760aec-1aa6-1e10-7da1-71808f893bf2
## 6 Semi-nat_6  AN09774     3c34ac4e-0788-50d9-083a-b8f304166fb0
## 7 Semi-nat_7  AN04095     53a2a769-81d0-6b51-0067-e50172392a45
## 8 Semi-nat_8  AN06685     6fc6939b-7a55-a074-103d-e7b9b3db09cb
## 9 Semi-nat_9  AN07399     e14b08a6-2b17-351a-4b7b-c9445dbea181
## 10 Semi-nat_10 AN05494     17d0299b-1faa-a090-4403-14b89881572c
## 11 Skog_1      AN01092     <NA>
## 12 Skog_2      AN00958     eacac0ce-c530-4f9b-937f-cf7cdc0a1064

```

##	13	Skog_2	AN00958	98f01570-3899-437c-bc48-b9355ecd77c3
##	14	Skog_2	AN00958	b17315da-ef8b-4ce3-b9f3-ab9f9a7fddde
##	15	Skog_2	AN00958	d0646269-56ad-453f-9ec3-261763560a69
##	16	Skog_2	AN00958	1ba7dd73-c290-458c-b90a-ec313ee56a24
##	17	Skog_2	AN00958	00151f09-c2ea-4904-bbb8-ee51d338e07f
##	18	Skog_2	AN00958	1d68691b-3139-4691-9267-7562ef6383c9
##	19	Skog_2	AN00958	d96414d1-f1bb-4cbf-b5b8-87fdbd42681b1
##	20	Skog_2	AN00958	74367c02-3c1d-4c3f-84d8-9c11a46adb9b
##	21	Skog_2	AN00958	438ae2c4-fa3a-4eb1-a77b-a5139189659a
##	22	Skog_2	AN00958	1eed14ae-2406-4e3d-9c13-b789ac047eee
##	23	Skog_2	AN00958	36d5710d-4f81-474c-8b84-6be1478004a7
##	24	Skog_2	AN00958	b277acfe-2984-4e77-939f-56749c3d3185
##	25	Skog_2	AN00958	0aace735-6935-415b-913c-44e2f5f68322
##	26	Skog_2	AN00958	8395488c-816c-4360-9525-18a16aaaf2e9e
##	27	Skog_2	AN00958	d625e9be-1839-4dcb-8546-750aae4efd44
##	28	Skog_3	AN00426	50d47680-b9fd-447d-9823-5fb7e2f0fa22
##	29	Skog_3	AN00426	9b6d609d-07d1-4e2f-92ba-14d60f09c2ff
##	30	Skog_3	AN00426	af4d5bf6-0687-47e5-8af8-568f511f8889
##	31	Skog_3	AN00426	4f122810-a082-4449-9c0c-6b5e60bf56f3
##	32	Skog_3	AN00426	7f1f588c-3d05-40ac-a706-8396530c4c9f
##	33	Skog_3	AN00426	bf617829-9a06-426d-b935-63570717a28c
##	34	Skog_3	AN00426	3a8edc11-afd8-4537-8da8-c902067c8d83
##	35	Skog_3	AN00426	bb8d62af-1f1c-4143-8e35-ade2259a5b52
##	36	Skog_3	AN00426	ba3f3fee-0612-4e4e-a076-990e792e2494
##	37	Skog_3	AN00426	4a93708b-6cd0-4a97-97bc-217482cb74d8
##	38	Skog_3	AN00426	82c85b12-b13c-4316-a0c3-9c6f2f54957a
##	39	Skog_3	AN00426	bb957353-9dac-4167-a3ea-41e34367571d
##	40	Skog_3	AN00426	d8f16f8b-01ae-430e-b5a7-163ee8f1cee2
##	41	Skog_3	AN00426	f6154d42-2f83-4464-a360-faac441a917a
##	42	Skog_3	AN00426	a4c5252f-92f2-4784-8a26-b9aff0f7dba8
##	43	Skog_3	AN00426	10663364-b8f5-48e2-921d-6b3fafd0ca77
##	44	Skog_3	AN00426	bad8d4b5-199f-4b07-af45-7cbfdffc99fa
##	45	Skog_3	AN00426	44fa14e7-6e64-40bc-98f8-d1bcce55895d
##	46	Skog_4	AN00574	6fbcb73f-d59b-4fc4-94f6-e6426f74d95a
##	47	Skog_4	AN00574	86319924-3495-4572-b01c-86d0ebab2417
##	48	Skog_4	AN00574	3adaf83f-d835-4a26-ab73-6ebac96af38b
##	49	Skog_4	AN00574	ebc51dc9-3842-4a20-8360-3a60c66abc5a
##	50	Skog_4	AN00574	1c2f25d0-2d5e-4aab-9724-cf84a125ff4a
##	51	Skog_4	AN00574	fa7381bd-4323-48b6-b3c4-0acbacin53c77
##	52	Skog_4	AN00574	373ac331-911c-4359-8b95-1623d19aa6dc
##	53	Skog_4	AN00574	0d3022e5-182d-4838-87c5-ad800511fcdd
##	54	Skog_4	AN00574	1427d114-6db8-4078-a673-82567b270251
##	55	Skog_4	AN00574	7fca1212-c746-45cc-89c4-ff68623bc25c
##	56	Skog_4	AN00574	9618245a-9c95-4807-a6cb-0c5dabe567db
##	57	Skog_4	AN00574	1efd2baf-fc92-4d32-8ac2-d63e11221f8c
##	58	Skog_4	AN00574	c6cb52dd-fa15-4679-969e-aac737feb040

## 59 Skog_4	AN00574	87535e15-9fb9-4966-8e25-6af45c4b07b
## 60 Skog_4	AN00574	eeb6f92c-b48b-4e9f-b47d-63e636cbccae
## 61 Skog_4	AN00574	f32db2c5-9446-48e2-8e55-d935af463f53
## 62 Skog_4	AN00574	8a281e97-f73e-4186-9253-855d6d0001d9
## 63 Skog_5	AN00800	cc27776b-2fdb-49ac-9a84-a0ada7c072c8
## 64 Skog_5	AN00800	b43fd424-9a27-42b5-97ce-31e48a8da2a8
## 65 Skog_5	AN00800	8f11d82c-327f-4417-9650-50d139b68acc
## 66 Skog_5	AN00800	5e58b79d-783e-49d2-8105-115d5ad3c97f
## 67 Skog_5	AN00800	8f472294-92cd-4c86-b563-f4023633646b
## 68 Skog_5	AN00800	6adeaa18-9172-4cfc-bfd4-4bf9d2d2d40f
## 69 Skog_5	AN00800	d8f5eb87-9fa1-41aa-8c7f-f4f6cabd784a
## 70 Skog_5	AN00800	558e0857-02b1-4e26-80a7-d7874af78fb7
## 71 Skog_5	AN00800	2e751260-2c79-4223-85f3-3b389b5dd623
## 72 Skog_5	AN00800	eae98d16-8b5e-40a4-afa7-93fb9f4493c2
## 73 Skog_5	AN00800	4b617538-df95-4ed6-87a3-45c324c765c7
## 74 Skog_5	AN00800	1b290a93-a182-43d4-aa5a-7a1c815fa4e3
## 75 Skog_5	AN00800	48de301a-6814-4ad1-ab8f-825b2f749929
## 76 Skog_5	AN00800	14d75cf1-b06c-4371-94fd-5c988771daf1
## 77 Skog_5	AN00800	4d4b70c8-5856-4348-a0fd-008927488d1b
## 78 Skog_5	AN00800	51ff49da-2371-4abc-b5e4-e30313de6108
## 79 Skog_5	AN00800	f9953dce-3264-43f0-a59e-ed6045ca3626
## 80 Skog_5	AN00800	6943555f-ae71-4210-8ebe-c1f6d628c415
## 81 Skog_6	AN00856	ad910f07-604e-41c6-b0d9-9cd8a31b2185
## 82 Skog_6	AN00856	2b4e63fb-319f-446d-9637-a0dc05a2604e
## 83 Skog_6	AN00856	9bb6eef8-8d05-435d-b1e0-8d8ab84681a7
## 84 Skog_6	AN00856	c4e7bdb1-6b6e-4dbb-ad46-e1dc64dccd4e
## 85 Skog_6	AN00856	6939e70b-6844-47f8-bcef-61c0b30bde87
## 86 Skog_6	AN00856	43fb5f6b-6d6a-44d8-8f2a-3dea56177674
## 87 Skog_6	AN00856	58ac69c7-e288-4f26-9bf5-0232183c4adf
## 88 Skog_6	AN00856	8eb7f451-82af-4c68-aeaf-770c2ee40f1a
## 89 Skog_6	AN00856	ced9ff6f-46e6-4225-b6b5-0fac3a4eb26c
## 90 Skog_6	AN00856	c34b72b3-2c0d-4a90-aab5-3469b685efe3
## 91 Skog_6	AN00856	094d7455-5849-45bb-818e-13d6d7a565aa
## 92 Skog_6	AN00856	0b345076-5109-40f6-9bd2-99324c1f541d
## 93 Skog_6	AN00856	cd32c1ad-efcb-4688-9509-b13c1eadb9e8
## 94 Skog_6	AN00856	a011438c-33a6-4ad7-aebb-1b64a34779a2
## 95 Skog_6	AN00856	034e1f5e-c02c-4465-849a-2937a59afaa0
## 96 Skog_6	AN00856	ad30cab3-8320-4905-9120-22915ac57e4c
## 97 Skog_6	AN00856	81e3fe2b-24b2-4208-aad7-614da78aed48
## 98 Skog_6	AN00856	180007e6-37f7-464b-804c-4a01f24cc680
## 99 Skog_7	AN00534	4b0f9cc3-4529-437e-b95b-2def395159b9
## 100 Skog_7	AN00534	c2a914ca-75ca-4a2b-88d3-c7eefdb86bea
## 101 Skog_7	AN00534	0ff427a1-1ec5-43b1-bb8d-f283f07b56b6
## 102 Skog_7	AN00534	ad708040-36e6-46c9-94df-ad1578bc3018
## 103 Skog_7	AN00534	d9a35b41-851a-44cf-9f2b-183a981f19cc
## 104 Skog_7	AN00534	b69221c3-6525-478c-878d-a4ae79c233d7

## 105 Skog_7	AN00534	e094d311-57fd-40f7-add9-c0a8f576c44e
## 106 Skog_7	AN00534	a8af17f8-ea1a-41cf-bc77-e548eb22a575
## 107 Skog_7	AN00534	ac84b604-b999-40ee-af2c-c3e3757c2b01
## 108 Skog_7	AN00534	f1369211-4763-414b-9704-3ab816340ef9
## 109 Skog_7	AN00534	8cc22e10-b412-4788-8c15-2015578b7e9e
## 110 Skog_7	AN00534	3a11ab54-aa71-431c-b7ec-a0d1f25c17f6
## 111 Skog_7	AN00534	b6fd6696-e5fc-4016-a8d0-a190d2825922
## 112 Skog_7	AN00534	a510b524-b803-472c-b311-1b5db9807595
## 113 Skog_7	AN00534	19fb1513-ef46-4a32-9f76-2cbdaccb6999
## 114 Skog_7	AN00534	6828fd28-2a82-4098-8244-354996b65c63
## 115 Skog_7	AN00534	fd53364a-f6b4-433f-b782-4f98f35754c7
## 116 Skog_7	AN00534	039d8eb8-779a-4c19-bbb1-ec62544c21cb
## 117 Skog_8	AN00051	397ab2fc-7719-4235-8fa9-f4937591f991
## 118 Skog_8	AN00051	d76b3990-0d7f-4915-8ad1-85b634536148
## 119 Skog_8	AN00051	6c249d32-46f1-4250-b060-db1d9e8de3ed
## 120 Skog_8	AN00051	3d32b4a0-3e4d-4318-ad24-4e84894aca08
## 121 Skog_8	AN00051	9327696f-407e-4938-b418-d6989d530a26
## 122 Skog_8	AN00051	8ae13c78-2821-48f7-8eae-8f5d271aa950
## 123 Skog_8	AN00051	1b69394d-c000-4a35-b403-33b64c9deb69
## 124 Skog_8	AN00051	4a06f6f3-d677-45ed-98b9-236c6972763d
## 125 Skog_8	AN00051	0c168294-1f84-47f5-a8a6-c06785bf46a0
## 126 Skog_8	AN00051	93605b59-a4e8-4d3e-8ff1-a55e19b67b8c
## 127 Skog_8	AN00051	829b6c69-ccbe-47ab-a9aa-0aa7ec31ef81
## 128 Skog_8	AN00051	4e01548f-5311-445b-be8c-adc57f98eb39
## 129 Skog_8	AN00051	dc8d0099-aa14-4f05-8869-afad40591484
## 130 Skog_8	AN00051	0a2250f4-16a0-48d9-85e0-1e8e8f7b3ec0
## 131 Skog_8	AN00051	a9417c27-0554-436e-94ca-4a1dfe4d7a8a
## 132 Skog_8	AN00051	324ba37b-160e-4413-ad23-c697fba387b7
## 133 Skog_8	AN00051	2ea4d8ff-06b2-4ea4-9525-810969d7beed
## 134 Skog_8	AN00051	d6e6b5e2-d9f8-49aa-b014-2796acd67417
## 135 Skog_9	AN00914	6fd9b9d2-7893-473a-8b67-a2ba398414a7
## 136 Skog_9	AN00914	f5b9b0fe-7b48-42e9-88a1-a8b3c04f488a
## 137 Skog_9	AN00914	8f15d6e3-97c1-458d-8b42-4d12362fdbfa
## 138 Skog_9	AN00914	95838ef7-551b-48d5-af85-15c0df6621de
## 139 Skog_9	AN00914	5c42ec16-88df-4323-80e5-571a980326cf
## 140 Skog_9	AN00914	98ee5314-56ec-4d86-94ae-bcab139e5249
## 141 Skog_9	AN00914	bac49f20-4048-4e00-a9a4-d07153e04bea
## 142 Skog_9	AN00914	d9c1aafb-41a7-469e-8454-ce9b8423962a
## 143 Skog_9	AN00914	a5868ed4-cd56-4367-a7c0-5c32ce3ad416
## 144 Skog_9	AN00914	d41ed974-ff53-4a64-b0cc-326d990374a8
## 145 Skog_9	AN00914	39f6b55f-ed5f-4389-8d8d-602b3baf1be8
## 146 Skog_9	AN00914	106ce33d-3612-4577-bd37-a09331a2044d
## 147 Skog_9	AN00914	f59861bf-ad43-4c2c-a032-f44a15ed8534
## 148 Skog_9	AN00914	9660d2c0-099f-4091-8ce2-d5debfa10c73
## 149 Skog_9	AN00914	737f80e4-c9db-4c3f-ae0a-23699803a968
## 150 Skog_9	AN00914	2e07c31a-4f0f-44df-b103-e7982bf09f92

```

## 151 Skog_9      AN00914      82f4e1bc-4746-4823-a1eb-4cdc83ccee43
## 152 Skog_9      AN00914      d962d6ac-be4e-4046-893d-9b94779e497c
## 153 Skog_10     AN00588      694fab07-c095-49ac-b64a-609a21ccc417
## 154 Skog_10     AN00588      6e0eba4e-0414-4e12-b0cc-ecc4939bb4cb
## 155 Skog_10     AN00588      ac660d80-ed6a-4d2a-9dc7-b7ac78ecc0fd
## 156 Skog_10     AN00588      9702fad8-81de-4a6f-8e69-fda7ecd517a1
## 157 Skog_10     AN00588      a299825e-dccb-4af8-95a9-2ccd260b254f
## 158 Skog_10     AN00588      bb0c08db-1a6a-4cad-a766-6bedaed5bc04
## 159 Skog_10     AN00588      2a4e885f-67fc-47da-ad3e-e32c8e72257f
## 160 Skog_10     AN00588      56800450-c3c7-4df6-a0f4-e71d69a36e15
## 161 Skog_10     AN00588      f43ebd65-a5ef-4d5b-9ab9-42bf205b2bc0
## 162 Skog_10     AN00588      21b60b22-89ed-46df-ae03-0b094defaf63
## 163 Skog_10     AN00588      007a3d44-309c-4863-b4bc-431809da3da3
## 164 Skog_10     AN00588      21d064e7-11ca-45f6-9136-681ef02d14c0
## 165 Skog_10     AN00588      47bdc52d-d8a5-43cd-8612-d41024c8db70
## 166 Skog_10     AN00588      65c73bf7-ea26-44b6-9749-326a9c54fb0a
## 167 Skog_10     AN00588      a83d70e8-29b1-4636-b503-22651f6c1b7a
## 168 Skog_10     AN00588      d07bc0e7-5aa1-452a-8b63-f2836ad71c7d
## 169 Skog_10     AN00588      facfc9d24-81f3-40cc-8ab5-4477e63b0844
## 170 Skog_10     AN00588      07b69d68-5258-4e98-ab1f-cb42dde616a

ano_herb_spec <- trap_loc %>%
  left_join(ano_plots,
    by = c("ano_flate_id" = "ano_flate_id")) %>%
  left_join(ano_arter,
    by = c("global_id" = "parent_global_id")) %>%
  select(-c(geom_punched, geom_inferred)) %>%
  collect()

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 4)

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 59)

ano_agg <- ano_herb_spec %>%
  group_by(global_id.x) %>%
  summarize(location = first(location),
            no_spec = n_distinct(navn),
            cover = sum(dekning_prc, na.rm = T)) %>%
  group_by(location) %>%
  summarise(mean_no_spec = mean(no_spec),
            mean_cover = mean(cover)) %>%
  collect() %>%

```

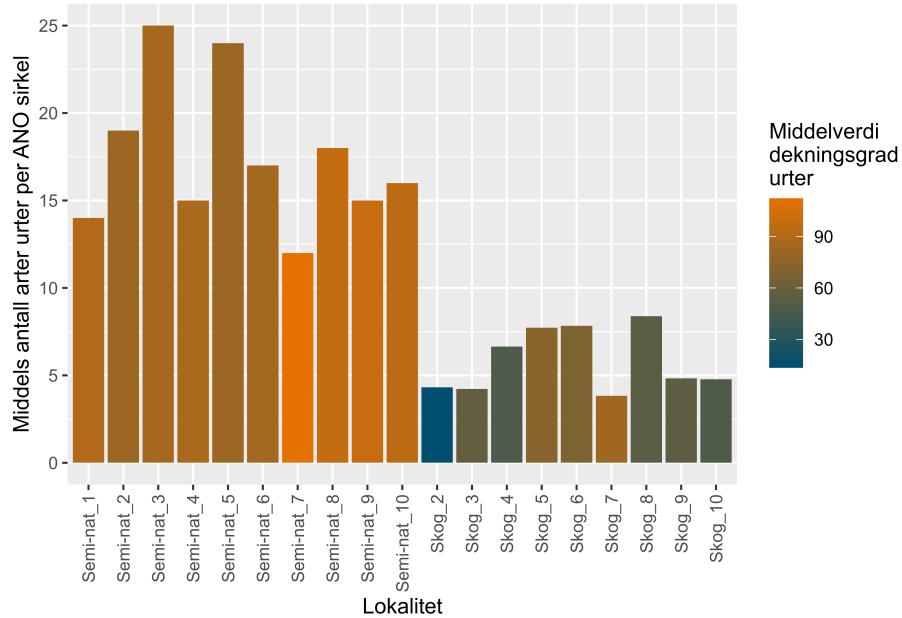
```

    mutate(location = factor(location, levels = c(paste0("Semi-nat_", 1:10), paste0("Skog_", 1:10)),
filter(location != "Skog_1"))

## `summarise()` ungrouping output (override with `.`groups` argument)
## `summarise()` ungrouping output (override with `.`groups` argument)

ano_agg %>%
  ggplot(.) +
  geom_bar(aes(x = location, y = mean_no_spec, fill = mean_cover), stat = "identity") +
  scale_fill_nina(name = "Middelverdi\ndeckningsgrad\nurter",
                  discrete = F,
                  palette = "darkblue-orange") +
  ylab("Middels antall arter urter per ANO sirkel") +
  xlab("Lokalitet") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))

```



Forest-registrations

Some simple graphs of the forest registrations.

```

tree_reg <- tbl(con,
                 in_schema("landsskog", "survey_data"))

```

```

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:

```

```

## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)
## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 1)
tree_plots <- tbl(con,
                     in_schema("landsskog", "survey_points"))

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)
trap_loc <- tbl(con,
                     in_schema("traps", "locations"))

## Warning in postgresqlExecStatement(conn, statement, ...): RS-DBI driver warning:
## (unrecognized PostgreSQL field type uuid (id:2950) in column 0)
tree_spec <- tree_reg %>%
  left_join(tree_plots,
              by = c("parent_id" = "id")) %>%
  left_join(trap_loc,
              by = c("ano_flate_id" = "ano_flate_id"))

tree_agg <- tree_spec %>%
  group_by(location) %>%
  summarize(no_spec = as.character(n_distinct(treslag)),
              avg_age = mean(alder, na.rm = T)) %>%
  collect() %>%
  mutate(location = factor(location, levels = paste0("Skog_", 1:10)))

tree_agg %>%
  ggplot(.) +
  geom_bar(aes(x = location, y = avg_age, fill = no_spec), stat = "identity") +
  scale_fill_nina(name = "Antall treslag",
                    discrete = T,
                    palette = "darkblue-orange") +
  ylab("Middelalder på de 2 største treene") +
  xlab("Lokalitet") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))

```

